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SOURCE
ORGANISM
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036N04 of
Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                2 (bases 1 to 900)
Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                           Saurin, W. and Weissenbach, J. Human gene number estimate provided Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                   1. (bases 1 to 900)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetie
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            CTTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTATAGGGTTAATACTT
                                           AAAAAAWATTTATTATAAAWAATAAAATAAATTMTTACAATATWTNATTATATTTT
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AATWATTTACWCTMTTATTAAWATTTTTTTTTTATCCACTTTTTTWWTNTTTTATCTTTTT
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/db_xref="taxon:99883"
/clone="036N04"
/clone_lib="c"
/clone_Lib="c"
/note="Genoscope sequence ID : C0BG036DG02LP1-end
1 154 c 115 g 340 t 65 others
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                                 AARAAAKKGKKGGGRKGGGAGGGRAAAAGATWTTWAKTDTTKTKAGDAKTTTTKKTTTWA
                                                                  TTTTAGGGTTTGGAATAGGTTCTTTTGCTCAAGGAGATATTCTTGGGGGGTTTTCTTATTC
                                                                                                                                    AACTTTTAGCTTATGAAACTAGTAAGAAAGATCCTATTGTGCCATTTTTATTGAACCTTT
                                                                                                                                                                                                   TTTCTAGCTTTGCTCAAGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAA
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                                                                                                   KKDKKAKKKKAAAKDAAAAAAAKKKDKKKDAAKAAAKKKKKDAAKKKKAKKKDDAWA
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
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/note="end : T7"
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/clone_lib="DrosBAC"
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/db_xref="taxon:7227"
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B1; Mismatches
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila the BDGP is constructing a physical map of the Drosophila and these BACs. For further informat
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                               TGGCAGGTGCAGTTACTATGGCTGTGACAAGATTGACAGAAATTATTATTCCGTTTACAT
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/db_xref="taxon:7227"
/clone="BACR29B23"
/clone_lib="RPCI-98"
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                                                                                                                                                                                                                        Local Similarity
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library or
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GTTTTTTCTAGCTTTGCTCAAGCTGATGATTCTAAAAAGCGCTTTTAATTTTGGGAGCGGGA 317
                                     AGTTTTAATAAAGAGGTTTTTATGAATAAATTTTTAATTGTTTGTTTTGCTAGCCTTTTGT
                                                                                                                    GCCTAGTTTTGATATTAATATGGGCCAAGCTAGCGCTCTTGGGTTTGAACTATCTTTCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BACR11P07 of RPCI-98 library from Drosophila melanogaster
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a NRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Ephydroidea; Drosophilidae; Drosophila.
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191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-98"
/note="end: TET3"
112 c 37 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila
/db_xref="taxon:7227"
/clone="BACR11P07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67.6; DB Pred. No. 0.018;
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Indels Length

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Gaps

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439 562

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559

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RESULT 7
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                                                                                                                                                                                                                                                                     KEYWORDS
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Best Local S
Matches 135
                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAGCTTATGAAACTAGTAAGAAAGATCCTATTGTGCCATTTTTATTGAACCTTTTTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAWATAAATATGWTAWTAAATTTTTTATKAWWAAAAAAWAATWTTTTWWTTTTTWAWAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135;
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                             Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Kluyveron
1 (bases 1 to 1167)
                                                                                                                                                                                                                                                                       GSS.
                                                                                                                                                                                                                                                                                                                                              CNS07360 1167 bp clone BA0AB017A09 of library BA0AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                           Kluyveromyces
AL427102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                          Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G
                                                                                                                                                                                                                                                Kluyveromyces lactis.
                                                                                                                                                                                                                                                                                       AL427102.1 GI:12210296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR27A24"
/clone_lib="RRCI-98"
/note="end : T7"
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32.0%;
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                                                                                                                                                                                     Kluyveromyces
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210 of
                                                                                   Potier, S.,
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MEDLINE
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                                                    422 TCTTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTATAGGGTTAATACTT
                                                                                                                      964
                                                                                                                                                         304
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                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                664 TGTTATTTATATTWTAAATWTBTWTBATWTTTKKSKTSSSSCCMANMMCABMVAAMAMWM 723
                                                                                                                                                                                                                                                                                             184
                                                                                                                                                                                                                                                                                                                                                                                                724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 TTTTCATTGGATCCCAGAATTTGTAGAATTTTCGACAAATAAAGACATTATTAAAAGAAT 63
                                                                                                                                                                                                                                                          CCTTTTAWWTTTTTTAAATTAAWAWTTAAWWATATTWWTTWWAAAAWWWTTAWATWTTT
                                                                                                                                                                                                                                                                                                                                                                                                                            TGAAATTGCTAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAA 123
                                                                        CATTTTATTGAACCTTT--TTTTAGGGTTTGGAATAGGTTCTTTTGCTCAAGGAGATAT 421
                                                                                                                                              TGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCAAGCTGATGATTCTAAAAGCGCTTTTA 303
                                                                                                                                                                                                                                                                                                                             TACTTTGAAAAAAGTTAAATTTAAATAGTTTTAAAAACCTTTTTTAAATTTCATTAATAT 183
                                                                                                                    195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: sequefigenoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   keywords for description of this sequence and for the sequence of the other extremity of this insert.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyce:
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS
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20584711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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117 c 96 g
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/strain="CLIB 210"
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/clone="BA0AB017A09"
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41.18;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neoteleostei
Acatinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodonidae; Tetraodon.
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                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
               Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizar
Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
Weissenbach, J.
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                                                                                    Fizames, C.,
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department o Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
Drosophila melanogaster
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ALO71865
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                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencaç
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns
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                                                           TDDTDADWWDWKDWDWKDADTKAGRKRGWGWKKGGWKKTTKTKKKKKTDKTKTGTDTKWG
                                                                                                         TTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCAAGCTGATGATTCTAAAAGCGCTTT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome survey sequence SP6 end of BAC BACNO3G04 of DrosBAC library from Drosophila melanogaster (fruit
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/note="end: SP6"
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/clone_lib="DrosBAC"
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/db_xref="taxon:7227"
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                                               120;
                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the
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    Web : www.genoscope.cns.fr)
    Détermination of this BAC-end sequence was

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="BACR08K10"
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/note="end : TET3"
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TGTTGTTTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCAAGCTGATGATTCTAAAAG

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                                                                                                                                                                                                                                                                                                                                                                                                            TAATTGTTGTTTTGCTAGCCTTTTGTGTTTTTTTTTTAGCTTTGCTCAAGCTGATGATTCTA
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Human gene number estimate provided by genome wide analysis using
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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## SUMMARIES

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17	17	17	17	17	17	DB
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AL071865 Drosophil	AL300850 Tetraodon	AL063921 Drosophil	AL098379 Drosophil	AL228940 Tetraodon	AL078714 Drosophil	Description

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## ALIGNMENTS

	COMMENT	TITLE JOURNAL	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 CNS00LT2 LOCUS DEFINITION
Collaboration with the Berkeley Drosophila Genome Project (BBGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial		Direct Submission Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  1 (bases 1 to 1101) Genoscope.	GSS. Drosophila melanogaster. Drosophila melanogaster	BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence. ALO78714 ALO78714.1 GI:5102004	CNSOOLT2  1101 bp DNA linear GSS 14-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC:

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                                                                      Designing primers and probes for analysing diseases associated cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified ge
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   TTTTGTTTATTATTATATTTT
                                                                   ATTAAAATGAGTGATAGCAATTTTGTATTGTGATTGCTCATTGTAATTGAAAATTAGAGC
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                                                                                     Chemically treated cell signalling
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The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell CC signalling, as well as oligonucleotides and/or PNA-oligomers for CC detecting cytosine methylations, as well as a method which is CC particularly suitable for the diagnosis and/or therapy of genetic and CC epigenetic parameters of genes associated with cell signalling. The CC chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences CC given in records ABL70111-ABL70626 represent chemically pre-treated CC Note: The sequence data for this patent is not represented in the printed Supecification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomisequences of genes associated with cell signalling -
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01-SEP-2000;
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Sequence 9742 BP; 2945 A; 88 C; 1819 G;
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4890 T; 0 other;
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Query Match 19 AGAATTTGTAGAATTTTCGACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTT Local 366; Similarity Conservative 44.0%; 7.68; 0; Score 65.8; DB 2 Pred. No. 0.0038; Mismatches DB 24; 462; Indels Length 9742; ω •• Gaps 2;

Matches 3615 79 TATGGTCAAATCAAGAAGCTCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGT 138

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CC Note: The sequence data for this patent is not represented in the printed CC specification, but is based on sequence information supplied by the
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                                            TGTGACAAGATTGACAGAAATTATTATTCCGTTTACATTTGCTAATAGTTATAATAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGTTAATACTTACAGGAGCTTATTTAGATATCAAAGCTCTTGATAAGAATGCTCCAAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITTGCTCAAGGAGATATTCTTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTGAGTGTTTGTAGTTTTTTAAGTGTATAGTGTAAGTTGTCGGTAGAATTAGTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTATGAAACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTATGTTTTATATTTAGGTTATATTGATGTAATAGGTGGGTTTTTATGGGTTTTTGA 4152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAAGAGGTTTTTATGA------A 223
                                                                                    ACTGAAAAATAGCCTTAATATAGCTTTTGGAGGGTTTGAGCCTAGTTTTGATATTAATAT
                                                                                                                                                                                                               --- GATTATTTTÄTTTTÄGTTGTTAATAAGTTTTTAATTTTATTTGAGATTATTATAG
                                                                                                                                                                                                                                                                                                      AGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                       h 7.8%;
Similarity 44.4%;
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6012 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1842 A; 43 C; 1153 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 0.0022;
0; Mismatches 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2973 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6012;
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RESULT 13
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                                                                         for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of disease associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK21545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4690
                                                                                                                                                                                                                                                                                                     signal transduction associated genes. The DNA sequences are chemical modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligomers
                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction \,
                                                                                                                                                                                                                                                                                                                                                         The present invention relates to chemically modified DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK31187
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antitumour; cytostatic; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2002
                                                Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an; signal transduction associated gene;
island; signal transduction associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATTTTTGGTATTAATTTATTGTATTAGTTTATTTTTA 4788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGTTTGTTTAGTTTTAAAGTTGTTTTTATATTTTTTGGGTATTTTTATAGTAATATT 4749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTTTTGTTTATTTATTTTATTTTCTCTGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-EP07472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                           24pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated disease; solid tumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation state;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementary
                                                   directly
                                                                 part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA #15
                                                                                                                                                                                                                                                                                                                                                                                                                                             genomic
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Query Match Best Local Similarity

Sequence

6012

BP;

1842 A; 43 C; 1153 G; 2973 T;

Matches

Conservative

0;

Mismatches

445;

Indels

10;

Gaps

2

44.48;

Score 67; DB 24; Pred. No. 0.0022;

DB 24;

Length 6012; 1 other

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                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the concegenes. Sequences derived from tumour suppressor genes and concegenes. Sequences with even numbered Seq ID numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                        Matches 364;
   4213
                                                                                                                                                                                                                4033
                                                                                                                                                                                                                                                                                      3973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electro format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences
                                                                                                                                            4093
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6012 BP; 1842 A; 43 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
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01-SEP-2000;
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07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is missing)
                                                                                                                                                                              171
                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                      TTATTAAAAGAATTGAAATTGCTAATTTATGGTCAAATCAAGAAGCTCTATTGGGAAGC 110
TATTGAGTGTTTGTAGTTTTTTTAAGTGTATAGTGTAAGTTGTCGGTAGAATTAGTATTT 4272
                                                                                                                                                                                                              GAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTTAAAAACCTTTTTTAA 170
                                                                                                                                                                                                                                                                                TAAATATATTAATTTTAAATGGGAGAAATTGGTTAAAATAAAGGGGGTTATAGATTTTATG 4032
                                  TGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTATGAAACTAG
                                                                  TAAATTTTTAATTGTTGTTTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCAAGCTGA
                                                                                                                                        ATTITATGTTTTATATTTAGGTTATATTGATGTAATAGGTGGGTTTTTATGGGTTTTTGA 4152
                                                                                                                                                                        ATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTTTTTATGA-----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                   7.8%;
44.4%;
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                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 22;
Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         1153 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                         2973 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                      445;
                                                                                                                                                                                                                                                                                                                                                                                   Length 6012;
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                                                                                                                                                                                                                                                                                                                                                     10;
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01-SEP-2000;
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                                                            WPI; 2002-154758/20
                                                                                Olek A,
                                                                                                                                                       29-JUN-2001; 2001WO-EP07471
                                                                                                                                                                                                WO200202807-A2
                                                                                                                                                                                                                    Unidentified
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                                                                                                                                                                             10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIGENOMICS AG
                                                                                Piepenbrock
                                                                                                                                                                                                                                                                     treated cell signalling DNA sequence complementary to#19
                                                                                                                          2000DE-1032529
2000DE-1043826
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                                                                                 Berlin
                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                 7.
                                                                                                                                                                                                                                                 cell signalling disease
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Claim

1; SEQ

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NO 38;

24pp+sequence listing; English

Nucleic acid, useful for diagnosis and therapy of diseases with cell signalling e.g. cancer, comprises chemically modsequences of genes associated with cell signalling -

ases associated modified genom

genomic

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RESULT 10
ABL32517
ID ABL32
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                                                                                    The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                        Sequence
                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                           Nucleic acid comprising fraction diagnosis and treatment
                                                                                                                                                                                                                                              WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                         (EPIG-)
                                                                                                                                                                                                                                                                                                              30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                              02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                            WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurofibromatosis;
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                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAACTTTTAGCTTATGAAACTAGTAAGAAGATCCTATTGTGCCATTTTTATTGAACCT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune system
                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                        5930
                                                                                                                                                                           SEQ ID NO 490; 32pp + Sequence Listing;
                                                                                                                                                                                                  methylation
                                                                                                                                                                                                                                                                   Piepenbrock
                                                                             The
             Conservative
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2000DE-1043826
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                                                        BP;
                                                                            present
                                                      2122 A; 24 C; 912 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis;
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                        44.18;
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                                                                            sequence is a
                                                                                                                                                                                                           fragment of chemically modified ment of diseases associated with
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            0,
                       Score 67;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene SEQ
           Mismatches 420;
                                                                           gene of the invention
                        0.0022
                                                      2872 T;
                                 DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                psoriasis;
                                                      0 other
                                Length 5930;
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            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               epilepsy;
bowel dis
                                                                                                                                                                                                             gene, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
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            Gaps
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ARSULT 11
ARAS46298
ID ARS46
XX ARS46
XX TUMOU
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cytosine methylation; ds
                                                             Human; tumour suppressor gene; one cancer; tumour; CpG dinucleotide;
                                                                                                                            Tumour suppressor gene derived
                                                                                                                                                                                                                           AAS46298;
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Homo sapiens
                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                    TTTTTAAGTTTTTTTTTTTTATTAAGAATTTTTTTATAAAGTAA
                                                                                                                                                                                                                                                                                                                                                                                                           AMATTAGAGCTTTTGTTTATTATTTTATTTTATTTTCTCTGCTAA
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                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                   6012
                                                                                    oncogene; antitumour;
                                                                                                                                 chemically modified sequence #20
                                                               single-nucleotide
                                                                                                                                                                                                                                                                                                                                                                                      4959
                                                                                                                                                                                                                                                                                                                                                                                                                                 862
                                                                 polymorphism;
                                                                                         cytostatic;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                    8181
                                                                                                                                                                                                                                                                           8121
                                                                                                                                                                                                                                                                                                                                  8061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                            8238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 925-931; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-081217/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyme disease.
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                 665
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les 229; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy of infections, particularly Lyme disease
AGCTTTTGGAGGGTTTGAGCCTAGTTTTGATATTAATATGGGCCAAGCTAGCGCTCTTGG
                                                                                                                                                                                                                                   TGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTATAGGGTTAATACTTACAGGAGC
                                                                                                                                                                                                                                                                         ATTACTTTTGAACATCTTTTATCTTTAGGAATAGGATCCTTTGTTCAAGGAGATTATAT
                                            TATTATTCCGTTTACATTTGCTAATAGTTATAATAGGAAAACTGAAAAATAGCCTTAATAT
                                                                                                  CGGAGGAGTATTATCAGGAATAGGAGGGCTCACAATTGCAGCATCCTACATCACTGGAAT
                                                                                                                               GGGTAAGGGAATGATGTTGGCAGGTGCAGTTACTATGGCTGTGACAAGATTGACAGAAAT
                                                                                                                                                           ----ATACATGACCGGGGATATTGGATTCGTTACAGAAAGCACAGCAACAGTAATAAC
                                                                                                                                                                                     TTATTTAGATATCAAAGCTCTTGATAAGAATGCTCCAAAAGCCGCTTTTAAGTGGACTTG
                                                                                                                                                                                                                 TGGTGGTGGTGCACTTGGCTCTCAAGTGCTTGGAGGAATACTTATAATGGCTGG---
                                                                                                                                                                                                                                                                                                    ATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGTTCTTTTGCTCAAGGAGATATTCT
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               BP;
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                       Preq. No. 3.56
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Score 88.2; DB 20; Pred. No. 3.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3595 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             4 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 9399;
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                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasth antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                        Clayton R,
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                                                                  Claim 1;
                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation,
                                                                                                                                                                                                                                                     White OR;
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burgdorferi
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RESULT 8
AAX20261
ID AAX2
XX
AC AAX2
AC AAX2
DT 04-M
XX
DE BOII

AAX20261;

AAX20261 standard;

DNA;

9399

ВP

04-MAY-1999

(first

entry)

Borrelia burgdorferi polynucleotide sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAGGTTCTTTTGCTCAAGGAGATATTCTTGGGGGTTTTCTTATTCTTGGATTTGATGCA
                                                                                                                                                                                                                                                                                                              GAAAGCGAAAAAGCAACCATACTAGCACCATTACTTTTGAATATCTTTTTGTCTTTAGGG
                                                                                                                                                                                                                                                                                                                              GAAACTAGTAAGAAAGATCCTATTGTGCCATTTTTTATTGAACCTTTTTTTAGGGTTTGGA
                                                                                                                                                                                                                                                                                                                                                                   CAAGATAAACTTGAAAAAGGTGTTGGAGTGGAGATATCGCGACTGTAA----TGAAATAT
                                                                                                                                                                                                                                                                                                                                                                                             CAAGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                      AATATGAAAAAATTTTCACATTAATATTAATTTTAGTTTAACAATGCAAATCTTTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTTAA 157
                        ATTAATAT 703
                                                                                                                                                       GTTACAGAAAGCACAGCAACAGTAATAACCGGAGGAGTATTATCAGGAATAGGAGGGCTC
                                                                                                                                                                                GCTCCAAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTT
                                                                                                                                                                                                           CTTGGAAGG----
                                                                                                                                                                                                                                     GTTGGTATAGGGTTAATACTTACAGGAGCTTATTTAGATATCAAAGCTCTTGATAAGAAT
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ATTGGAAT
                                                  AACGCAGACCTTAAAAAAAGGCTCGGCATTGCACTTGCGGGGGGTTGAACCCAATTTTGAC
                                                                  AATAGGAAACTGAAAAATAGCCTTAATATAGCTTTTGGAGGGGTTTGAGCCCTAGTTTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1761 BP;
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Pred. No. 2.5e-(
); Mismatches 3
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RESULT 6
AAX20266
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AC AAX2
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DT 04-M
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DE BOII
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Best Local S
Matches 409
                          Borrelia
                                                  04-MAY-1999
                                                                          AAX20266;
                                                                                                 AAX20266 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can all be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page
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                                                                                                                                                                                                                                                          GGCTGTGACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAG
                                                                                                                                                                                                                                                                        GGCTGTGACAAGATTGACAGAAATTATTATTCCGTTTACATTTGCTAATAGTTATAATAG
                                                                                                                                                                                                                                                                                                                       AAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTACTAT
                                                                                                                                                                                                                                                                                                                                                                     TATAGGGTTAATACTTACAGGAGCTTATTTAGATATCAAAGCTCTTGATAAGAATGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTTTTGCTCAAGGAGATATTCTTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGG
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                                                                                                                                                                                 TATGGGCCAAGCTAGCGCTCTTGGGTTTGAACTATCTTTCAAAAAAAGTTATTAA 755
                                                                                                                                                                                                                                                                                                                                                         TATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTAA
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)B; AAY19809.
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                        burgdorferi polynucleotide sequence
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nilarity 86.1%;
Conservative
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 spirochete;
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Pred. No. 7.5e
0; Mismatches
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bacterium;
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ies 66;
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Best Local
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belong to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic endemic relapsing fever, and Lyme borreliosis, more commonly known
                                                     3276
                                                                                                                                                             3162
                                                                                                                                                                                                                  3102
                                                                                                                                                                                                                                                                        3042
                                                                                                                                                                                                                                                                                                                           2982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7074 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayton
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyme disease.
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                          398
                                                                                                                                   278
                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                   39 CAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGCT
                                                                                                                                                                                                                                                                                    CTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAGTTAAATTTTAAATAGT-TTTAA 157
AGGATCCTTTGTCCAAGGAGATTATATTGGTGGTGGCGCAGTGCTTGGATCTCAGTTATT
             AGGTTCTTTTGCTCAAGGAGATATTCTTGGGGGGTTTTCTTATTCTTGGATTTTGATGCAGT
                                                                                                                                                                                       GGGTTTTTGATAAATTGCATTAATATTTAATTATTAAAATTTATTGGGAGGTAATATCAA
                                                                                                                                                                                                                               AAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGGTTTT
                                                                                                                                                                                                                                                                                                                          CTAATAGAGGATCTCTATTGATATCATCAAAAAGTATTTAAAAATCAAAAATAAACCTAT
                                                   ACAAGATAAGCTTGAAAAAAGTGTT-----GGAAGTATTGAAACCATTATGAAATATAA
                                                                                                                                   AGCTGATGATTCTAAAAGCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTATGA
                                                                                                                                                             TATGAAAAAATTTTAACATTGATATTAATTTTTAGCTTAACAATACAAATCTTTGCAAC
                                                                                                                                                                                                                                                                     TTATTAACAAACTCATCTTAACCCAAATTTCATAGAAATTATAGTTTAAGTATTCTTTGG
                                                                              AACTAGTAAGAAAGATCCTATTGTGCCATTTTTATTGAACCTTTTTTAGGGTTTGGAAT
                                                                                                                                                                                                                                                                                                                                                                               410;
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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burgdorferi (Bb). Products derived from Bb can be used for
ction, diagnosis, characterisation, prevention and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 951-955; 1128pp;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dougherty BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                3064 A; 906 C;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 2233 T;
                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
.6e-09;
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                                                                                                                                                                                                                                                                                                                                              03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                             New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                    (HUMA-)
                        This
                                                                Claim
                                                                                                                                                                                                                                               Choi GH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigenic protein; vaccine;
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    This sequence encodes a Borrelia invention, which is suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    661
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DB; AAY19808.
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97US-0053377.
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  burgdorferi (Bb) protein use in a vaccine. The Bb
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03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                                                                  30-DEC-1998
                                                                                     W09859071-A1
                                                                                                       Borrelia
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Best Local
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  Borrelia;
                   Borrelia burgdorferi B31 protein encoding cDNA
                                          17-JUN-1999
                                                               AAX30098
                                                                                  AAX30098 standard;
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P13 antigen; spirochaete; vaccine; infection; diagnosis;
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                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a Borrelia burgdorferi B313 protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polyclonal antibody raised against a 13 kDa polypeptide of CC Borrelia burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC to ther spirochaetes. (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such CC (I), (II) are also used to produce recombinant (II). The 13 kD protein CC is involved in virulence and is highly conserved within B. burgdorferi CC sensu lato, but is absent from other Borrelia species (e.g. those CC responsible for relapsing fever or avain borrelosis). It should provide CC a more specific and sensitive antibody response, and diagnosis, CC compared with use of whole bacteria as antigen.
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid from Borrelia burgdorferi encoding virulence protein {\sf P13}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-215027/18
P-PSDB; AAY04278.
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                                                                                                                                                                                                                                                                                                                                                Sequence
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10-SEP-1997;
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                   TAAAA---GCGCTTTTAATTTGGGAGCGGGAGAAAAACTTTTAGCTTATGAAACTAGTAA
                                                                        TTTAATTGTTGTTTTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTTGCTCAAGCTGATGATTC
                                                                                                                                 AATTTCATTAATATGTTACTATAAATACCAGTTTTAATAAAGAGGGTTTTTATGAATAAATT
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                                                                                                                    AATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAACT
                                                            TTTAATTTTTGTTTTGGCAACCTTTTGTGTTTTTCTAGCTTTGCTCAAGCTAATGATTC
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97DK-0001041.
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88.4%;
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Gaps

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347

GAAAGATCCTATTGTGCCATTTTTATTGAACCTTTTTTAGGGTTTGGAATAGGTTCTTT

406 300 346 240 289 180 229 120 169 60 109

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SXCCC
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Matches 862;
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                                                                                                     GAGCTTATTTAGATATCAAAGCTCTTGATAAGAATGCTCCAAAAGCCGCTTTTAAGTGGA
                                                                                                                                                        TTCTTGGGGGTTTTCTTATTCTTGGATTTGATGCAGTTGGTATAGGGTTAATACTTACAG
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AAATTATTATTCCGTTTACATTTGCTAATAGTTATAATAGGAAACTGAAAAATAGCCTTA
                                     CTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTACTATGGCTGTGACAAGATTGACAG
                                                                                         GAGCTTATTTAGATATCAAAGCTCTTGATAAGAATGCTCCAAAAGCCGCTTTTAAGTGGA
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Pred. No. 1.8e-146;
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The present sequence encodes a Borrelia garinii IP90 protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polyclonal antibody raised against a 13 kba polypeptide of CC rabbit polyclonal antibody raised against a 13 kba polypeptide of CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC other spirochaetes. (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such CC infections, in standard immunoassays or amplification/hybridization CC tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi CC responsible for relapsing fever or avain borrelosis). It should provide
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10-SEP-1997;
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DB; AAY04280.
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97DK-0001041
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10185.565 Million cell updates/sec
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Borrelia burgdorfe
Borrelia burgdorfe
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Borrelia garinii I
Borrelia burgdorfe
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Human metastasis a	Human immune syste	Human immune syste	Human metastasis a	Human immune syste	Borrelia burgdorfe	DNA transcription	Human immune syste	Chemically treated	chemi	Human immune syste		Signal transductio		Human metastasis a	Human immune syste	Human gene regulat	Human chemically p	Ð	Human chemically p	Tumour suppressor	Human immune syste	Human immune syste	Human immune syste	Human angiogenesis	Human immune syste	Human gene regulat	Human immune syste	Chemically treated	H		Chemically treated	Signal transductio	D)	Tumour suppressor	Human immune syste

## ALIGNMENTS

Borrelia afzelii ACAI protein encoding cDNA

17-JUN-1999 (first entry)

Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis; ss.

AAX30099;

AAX30099 standard; DNA; 862

ВP

RESULT 1
AAX30099
ID AAX3
XX AX3
AC AAX3
AC AAX3
AC BOII
XX BOII WPI; 1999-215027/18. 16-SEP-1997; 10-SEP-1997; Bergstroem S; 04-SEP-1998; 18-MAR-1999. W09912960-A2 Borrelia (SYMB-) SYMBICOM AB afzelii. 97US-0059036. 97DK-0001041. 98WO-IB01424 /\*tag= Location/Qualifiers 219..755

This Pack BLAMK (USPRO)

CDS

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Local Similarity
ACAAATAAAGACATTATTAAAAGAATTGAAATTGCTAATTTTATGGTCAAATCAAGAAGC 97
                                                                                                                                     TCTATTGGGAAGCGAATTTCAAGTAATACTTTGAAAAAAAGTTAAAATTTAAATAGTTTTAA 157
                                                                                                                                                                                                                                                                              --AAACCTTTTTTAAATTTCATTAATATGTTACTATAATACCAGTTTTAATAAAGAGGTT
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MKHAQLEYEKQVEQQKRSVDFKEQVLNEKSRTTSKNSEYSSFYAQTIALTQROLSIT
WGDKFTLTSRELTILVLSFIFGGIYFQQPLTTDGLFTRGGALFTSIIFNCTLTQGELH
GALSGRRILQKHKSYALYRPSAYFVSQILIDIFFILVQVFLHSFIVYFMYGFEYRADK
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FFIFCFTLVGVSLSSASLFRGFANFTPSLFTAQNMFVFIFEVNYFGYSQTPDKMHS
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IEGSLSVKGENYLWDALQINSDHRALNVVVIFLFWLFYIGLNLFAVEYFDWTSGGYTH
KVYKRGKAPKLNDVEEERNONOIVKKATDNMKDTLKMRGGLFSWKSISYTVPVAGTNK
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GDIEVDPDNNNNFDITASPTSGGIKQLNIRTSYNGIVNEDDDRMLLGIVYWKNTSEGP
PGCVHGGALASMFDDSMACCIRYFYNNNFDDLNLQKQKQKQKQQQQEQEQPQGNRNGI
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LGSLVGSVENLRNLSTINSVPLILSPYEIRLGLEKQWFQIINESATFPTITDHNLSLF
KESRQTYYQSLMDKYKEQRLKKEKEFRNKLNTNSNSNKNKNKNKIPSLDTTDSNNNNN
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DLQVDGKQAPPREFANGFLTQFIEVYKRLNIIYYRDVFYTMGSFAQSAVSGLVIGFTF
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/protein_id="AAM43694.1"
/db_xref="GI:21166077"
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TAACTATTTAAATTTTTTTTTTTTTTTTTTTTTTTAAT 18977
                                                               ATTTTATTTATTATAAAATGAGTGATAGCAATTTTGTATTGTGATTGCCCATTGTAAT
                                                                                                                             TAATAGGAAACTGAAAAATAGCCTTAATATAGCTTTTGGAGGGTTTGAGCCTAGTTTTGA 694
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Search completed: March 27, Job time: 2281.68 secs 2003, 03:11:15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum.

Dictyostelium discoideum

Dictyostelium discoideum

Dictyostelium discoideum

Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

1 (bases 1 to 129360)

Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, Gloeckner, G., Eichinger, L., Szafranski, T., Szafranski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 129360)
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Lehmann,R., Baumgart,C., Parra,G., April,J.f., Guigo,R., Kumpf.
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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HTG; HTGS_PHASE2
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
/protein_id="AAM43687.1"
/protein_id="AAM43687.1"
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complement(join(2740..3021,3124..3357,3454..3626,
3750..3794,3908..4157))
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/note="ORF_ID:dd_02309"
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/db_xref="GI:21166069"
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                                        /product="hypothetical protein"
/protein_id="AAM43688.1"
                                                                                                                             /note="ORF_ID:dd_02313"
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                                                                                                                                                                                                                                                                                                                                           /note="ORF_ID:dd_02312"
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_xref="GI:21166071"
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complement(join(15910.
16502. 16576,16692. 1
note="ORF_ID:dd_02326"
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NEHFFTIVRSSSTSGGGSSNNNDESTDSITSBDLKQQHKVLLKNVHTIHNIENVQPTT
PTTTTSTILONGENRCLDENBOLOGOETEGOOSKKYKSTSKSBILNNLGSEYHDDIH
LQNIYIAHQKYHRVTIADSFKNIFCTLIPVKRFCY
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EKLNRNSNGGYVELTPISQSKRQRKNIGNRLVRPCDCKGTQRHVHVKCLCEWIGKCNK
WYCSICHRVYNLSPHHLHYCVMKLQRKGVLKNLPPIYSNTEFSRSSYFALLIFMGTLS
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RIETVNYLLSNYLQELTNQGPLKTYYTIFQFNNLSILNIFLSNEIYKSLLALYEINSE
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                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAM43691.1"
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join(13528. .13795,13916. .14022)
/note="ORF_ID:dd_02320"
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NGGIISFSNEVSGGGMFMNYNPLVGINGDTTTAGYNPGFLNSPSVSYYSFYPSSSSPS
IYISSTGGSSSAAQLNFHQHYNVNSIQSNNNKNKNNNKNDNNNDNNNINKKKKKKKKKKL
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ELKKINLIVEYFIEYDEILDDIEYQAINPNANGNSNDSGSNDSNDSGSGIDNNFNNKL
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/protein_id="AAM43690.1
/db_xref="GI:21166073"
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/note="ORF_ID:dd_02315"
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LRGHLKGTPLNKSPSFKDENIAASINIGVHGSKFESNATNTSQSTFFPEWKAPSFERN
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                                     GAGCTTTTGTTTATTATTTATTTTATTTCTCTGCTAA
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                         GAATTTCAAGTAATACTTTGAAAAAGTTAAATTTAAATAGTTTTAAAAAACCTTTTTTAA 170
                                                                          TTATTAAAAGAATTGAAATTGCTAATTTATGGTCAAATCAAGAAGCTCTATTGGGAAGC 110
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TAAATATAATTTAAATGGGAGAAATTGGTTAAAATAAAGGGGTTATAGATTTTATG
                                                                                                                                                                                                                                                                                    artificial sequences.

1 (bases 1 to 6012)

Olek,A., Piepenbrock,C. and Berlin,K.

Diagnosis of diseases associated with tumor suppressor genes
                                                                                                                                                                                                                                                                                                                                                                                Sequence 20 from Patent
AX251052
AX251052.1 GI:15984475
                                                                                                                                                                                                                                                                                                                                            synthetic
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo 43 c 1153 g 2973 t 1 others
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1. .6012
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                                                                                                                                                   synthetic construct.
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                                                                                      Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with signal Patent: WO 0200926-A 30 03-JAN-2002;
                                                                          Epigenomics AG (DE)
                                                                                                                                         artificial sequences
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genom
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Epigenomics AG
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                                                                                                                                                                                                                                        /note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <2233-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 949.980-seq 04 900.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001 1.849.980-seq 07 1.800.001 2.149.980-seq 08 2.100.001 2.449.980-seq 07 1.800.001 2.149.980-seq 10 2.700.001 3.649.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.649.980-seq 13 3.600.001 3.673.778 <2233-cOriginal length of seq 2: 3.673778 <2233-split as follows.-seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16 600.001 949.980-seq 17 900.001 1.249.980-seq 18 1.200.001 1.549.980-seq 19 1.500.001 1.849.980-seq 20 1.800.001 2.149.980-seq 12 1.000.001 1.849.980-seq 20 1.800.001 2.149.980-seq 21 2.100.001 2.449.980-seq 20 1.800.001 3.49.980-seq 20 3.700.001 3.649.980-seq 20 3.000.001 3.669.980-seq 20 3.000.0
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join(22390. .23275,24040. .24056)
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NEQANNAAMEKVRLDKQREVRAGHDGTWVAHPALIPIAMEQFNTHMKSQNQISYIPSS
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LNNSNNSVNSNNTPSQYHHHHHHHHHHHNNNSSSSSSSSGSSSTNGNNSSGGGGGGS
GSSSNSVDIIQASTPSSNNSGGINIIIPNPMSTNTIPPPNYGDSMMYNDPFFERKNSI
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/protein_id="AAM33219.1"
/db_xref="GI:20976630"
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complement(24572...24778)
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sfissfkktkkQaQaacsQLildyyyQdsnyksLQdkhkIsQQPQhnnGfsypkrdyn
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/protein_id="AAM33218.1"
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ITATKEALEDYNRYQSDKKNNLEPYTIVRDAKLETISSQDICVGDIIRIQNGQQIPAD
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                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          844
 Score
 67.4;
 BB
                                                                                                                                                                                                                                                                                                         DNA
 6
                                                                                                                                                            immune system
 Length 14950;
                                                           DNA
                                                        (Homo sapiens)"
                                                                                                                                                                                                                                                                                                          PAT 01-FEB-2002
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KEYWORDS
SOURCE
ORGANISM
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AC116965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18*MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biotechnology, Beuter 3 (bases 1 to 43993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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43993 bp DNA linear HTG 18-MAY-2002
Dictyostelium discoideum chromosome 2 map 497421-541412 strain AX4,
**** SEQUENCING IN PROGRESS ***, in ordered pieces.
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AC116965.1 GI:19920064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gency: Deutsche Forschungsgemeinschaft (DFG). MOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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3843. .3863))
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                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical
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2.1"
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6373. .640
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LNSGAKVFMADFEDANCPNWENSIHGQQNMIDANNRTISFTSAEGRKYELNKQVAVLF
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/note="ORF_ID:dd_01214"
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join(7448. .7866,7957. .7975)
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VISSLTLFPDYHPSKINARLKKEFSLNTKTIEEFERCKAISLAEAVTLVDKNKNNNNN
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SIATYKILFANRELYPMLNKLKGMISHLNKSQDVLISNHAEYYLNVLKGEYIPPVGNI
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join(4050. .4434,4547. .4897,5078. .5463,5559. .6079,
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complement(5803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \begin{minipage}{llll} ASYITGIIIPFKFANRYNADLKKRLGIALAGLEPNFDIGINGDSNYRLKNPIEYQFTW\\ G" \end{minipage}
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PID:580906 GB:AL009126 percent identity: 54.17;
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5069...5830)
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complement(5069...5830)
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58.62; identified
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SLSILMQTINDIKDFRNKSFWISILENQFLKNRNTFKDVEELLYKEYSFYIKGKIHYY
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/translation="MDRKESNIITIASPKGGVGKTTLTILFSYILKDLSKKVLLIDLD
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CKEDTKRACYILERLFFTKKEVLSDLINEYEKYKRKKKNKNKYLIFIIYGAIVILGWM
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LKYNLKDDIDNKIERMKILYEIKKKELYKYDNFSSFEQFIKHFVIAKTQAYLYLKVYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
/protein_id="AAF07708.1"
/db_xref="GI:6382398"
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3623. .4108
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Local Similarity
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                                                                                                                                                                                                           GGGTAAGGGAATGATGTTGGCAGGTGCAGTTACTATGGCTGTGACAAGATTGACAGAAAT 604
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                      AGCTTTTGGAGGGTTTGAGCCTAGTTTTGATATTAATATGGGCCAAGCTAGCGCTCTTGG
                                                                                        TATTATTCCGTTTACATTTGCTAATAGTTATAATAGGAAACTGAAAAATAGCCTTAATAT 664
                                                                                                                                                                                   CGGAGGAGTATTATCAGGAATAGGAGGGCTCACAATTGCAGCATCCTACATCACTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                         TGGTGGTGGTGCACTACTTGGCTCTCAAGTGCTTGGAGGAATACTTATAATGGCTGG----
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VEAGGEDDLYGICIDIDEFSKTATIVPITNNFEGYLVAKDSTLKVKDKLVFNKDGALE
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QMGYQRTVKWDAFLNANPTTIANEVNTISTIGFSSEVVRLNYLKLQYKFRHLKQASEK
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/protein_id="AAF07740.1"
/db_xref="GI:6382430"
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/protein_id="AAF07739.1"
/db_xref="G1:6382429"
/translation="MIVNESERAYALIAVGGPPPALIITPLLFINYKDENKHLKYDYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FYTSDSYLGDINNNLLPFSQAYKLASSEIIKLINHFVLTGTVSIQKDGKNQKRLLPNM
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/protein_id="AAF07711.1"
/db_xref="GI:6382401"
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identified by sequence similarity; putative"
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); Mismatches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAATAGATAGCATAATTTCAAATTTAAAAAGAGTTTAATGAAAACTTTACATTAAAAATC
Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B., Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D., Hickey,E., Gwinn,M., White,O. and Fraser,C.M.
A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease
                                                                                                                                                                                                                                  Borrelia
AE001584
                                                                                                                  burgdorferi group
                                                                                                                                                         Borrelia burgdorferi
                                                                                                                                                                                                                    AE001584.1
                                                                                                                                      Bacteria; Spirochaetales; Spirochaetaceae;
                                                                                                                                                                             Lyme disease spirochete.
                                                                                                                                                                                                                                                                        AE001584
                                                                                                 (bases 1 to 52971)
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                                                                                                                                                                                                                                               52971
burgdorferi plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein; identified by Glimmer; putative"
                                                                                                                                                                                                                  GI:6382393
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Pred. No. 1.7e-05;
0; Mismatches 326;
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1р56,
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                                                                                                                                                                                                                                                     complete
                                                                                                                                      Borrelia;
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                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                               plasmid
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                                                                                                                                      Borrelia
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                                                              Haft,D.,
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MEDLINE
PUBMED
REFERENCE
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JOURNAL
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Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Lathigra, R., White, O., Dodson, R., Hickey, E.K., Gwinn, M., Peterson, J., van-Vugt, R., Palmer, N., Haft, D., Rosa, P. and Stevenson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-NOV-1999) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spirochete Borrelia burgdorferi
Mol. Microbiol. 35 (3), 490-516 (2000)
20138354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/transl_table=11
/product="hypothetical |
/protein_id="AAF07738.1'
/db_xref="GI:6382428"
                                                                                                                                                                                         /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:520778 percent identity: 93.50; identified by sequence similarity; putative;protein p23, authentic frameshift"
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/protein_id="AAF07705.1"
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IVTEGIFSSLKLYASEHRLLVEIKKTLISLKDPNYRDVPPVRDYNEEYFNKFFLDLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="BBQ03"
856. .1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to
67.53; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="
279. .5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /plasmid="lp56"
279. .548
                                                                                                                                    /gene="BBQ05"
2744. .3496
                                                                                                                                                                         similarity; putative; protein 2744. .3496
   /product="antigen, P35, putative"
/protein_id="AAF07706.1"
                                                              identified by sequence similarity; putative" /codon start=1
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/note="similar
                                                                                                                                                                                                                                                                                                          TAYQQYLKVKREIERNTINGKIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:L31615 GB:L31418 PID:520783 PID:551742 percent identity: 97.81; identified b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GYLGVHRFYVGKIGTGLLYLFTFGFLYVGVLIDLIRITTNKFKCN*
                                                          /codon_start-
                                                                                                                                                                                                                                                                   /gene="BBQ04"
                                                                                                                                                                                                                                                                                          1404.
                                                                                                                                                                                                                                                                                                                           EQSKDLIKLFGRVKNEQNNKFKSEVYWLYSCISELYSPDIKYSGEEGSPEYDRFMPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BBQ03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BBQ02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTKYIAILVARFKKDAEICISCGVRNKQTENYNKLIVFLLCLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:6382394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
/protein_id="AAF07704.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Borrelia
/db_xref="taxon:139"
                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BBQ01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:U03641 PID:458212 percent by sequence similarity; putat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     burgdorferi"
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/gene="BBG04"
complement(2750.
/gene="BBG04"
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1047. .
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FFDTAQKRLKESIIKRLESKNNRSYYALELSRQALSDARSALSSLESFAFKRAEPMVR
KKKIKELIKHAKTVLESLNKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="This region contains an authentic frame shift and is not the result of a sequencing artifact.; similar to GP:2239281 percent identity: 63.64; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQEDSETPERVKKENFKNKFRHFLDVKYNKKFTAEEILGYIYAILYSNIYRDRFYEHL
QIDFPKIIFVDNSDIFVTLGKLGTDLINSHLVKVVPTININIGKCFSFLDETLKQNSI
IEKVFYKEETNELYYNQTSRFINVSKEVYNYTIGSWQTLKSYLTYRKGREMPSKEVEH
/note-"similar to PID:1143398 PID:1174342 PID:1174350 PID:2182755 percent identity: 57.84; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BBG06"
4208. .5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity; putative;transposase-like
frameshift*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:2228714 percent identity: 99.12; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="B. burgdorferi predicted coding region B
/protein_id="AAC66074.1"
/db_xref="G1:269031"
/translation="MKQEAISIIFDLEIAVHIKTLDINLNLIYNINGVV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity; putative; conserved hypothetical protein,
authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEKVIKTIHYTIGIQKK"
2104. .2495
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/translation="MEINLQSKLNNKNNNKLIFFISCSLVLVSTRPFDNRFTYYSKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to PIR:A64689 percent identity: 35.78;
identified by sequence similarity; putative"
/codon_start=1
                                                                                                                                                                                                                                                                   LLSTLAYVNSKYNKYTQKNILYCFNENLKRNGQPTTTLRTMQNYLYKLEKVFKYTTNY
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LVECLNNKNNNIKEERKI 10,1 EKYQVIKYFNKCNFSLLKEILPTLNLD) INKOELLKIL
KIIKRIEINLTKNKNTYLNVSYFKEKQNKLKKILSNTQQQLEKNGYNPEQLEISFQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2891. .4056)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="BBG03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BBG06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BBG05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11
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                                                                                                                                                                                                                                              ENYKTKPHFIIENHKYKDLSHIKRKLEKSIERKKENLQKDCENMRTNIFNILIEQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-"similar to"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:U03641 PID:458216 percent identity: by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predicted coding region BBG04"
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gene

CDS

gene CDS

complement(10776.
/gene="BBG11"

/gene="BBG11"

gene

CDS

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/translation="mdrkklakkphilaiasikggvgkstssimfstilsktinkvllv
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akfskegnofkelmlrnavynyledydyvildtppslsseldnalviabkviipvple
rwavemlpllingikelmnymgkeakiihifaskvelgrvtsteimslikekylnkf
igevhksealkkiidyaigekenenyvkeylrileki"
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/translation="MOMMAKGICVKETVRCSNKKDLEIKIEKDNDKTIYHTKIMMDI
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VGGIEKSYSLSKTYYMEVRFKKGSIFCYFKSLPRILKKENVNTTYNKALFSMFTTLER
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irnkintmkilleirnrklyildgykkfedfifdfkiartqaykyikiaklifegkle
eidiiengidktlfnlmkdkkinskanlitplrvrletqeacdfykmnpkfanyiled
fyqknkeqlikkleyknkqxys"
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6737. .7288
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5911. .6678
                                                                                                                         KMASKIQAMYKKFVDEHKSQFKKLNETNRNTIKOYAEKAQDITKSLYDSMIDGLNVFK
NAFMKDIAGKFLNKDTGESIGEEFHNLINGKDVNWGEGLEKMTTQMYESWKTGLKTAA
GAVFGPWGENVAELINGLTDFVWGILKGQEKARIKAIEKKDEDLEELEKRSEVELKK
                                                                                                                                                                                                                                NLVTFWKKAEKEKDTSGSEPERDKKEDPNAKTNINKKMAEDVOKLODETFNRORDIYN
KTGKAEQALKNLEKTINEKNEKFKDEYSKIFDOLTDENKLUGVEKSVNEENNSMU
DFVNEYQNLLKEKESREEIIKTLPHFDQVSALQKLNDEINEKNKAFVEKYGKSSEETL
NESNRQVYVALEKQVNEYEKTALDRSFVEAQKALQKEITDLEMETMLLPAKERASAEK
                                                                                                                                                                                                                                                                                                                                                                                                        AGGSSEGLEKLAEVYSRVESSNQVNLEDLYALRDAGVDITDILAEEAGLAGEALYKAA
SDGKIGFDALNKALSKATSEGGKFYGNTAKEAKTLAQAQQQTAKMSEKLFLDIGKALE
PMMIGFEKVKQFLMVALMVPLIKVTTATIYLTTKLGELVAYLAGKWVQGNKMLFKATI
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SVKNLANKTGEAFNOMLAAFAP I IMAVKA I QA I GSTI SG I FDGAMDALDEFNEEVSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein; identified by Glimmer; putative" \label{eq:putative}
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/gene="BBG10"
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/gene="BBG10"
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/gene="similar to PID:1143400 percent identity: 43.68;
/note="similar to PID:1143400 percent identity: 43.68;
identified by sequence similarity; putative"
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/protein_id="AAC66056.1"
/db_xref="gI:2690013"
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                                LEDRFDEEIKMRKEKLSELDDEYTKEIEFLKQAQSKGQISGEEFQKRLHDVQTEYKTK
KDIETTQLTKTEEAKKLEVERKNKLSKLEPERIKAQAEVDKVNAEDWWNLGKPDRLRK
TQKILDEILKRIAKVKSAGSIEEIKLAHGGARFVSNKPTYMPNSGVMSSEFGQPELVR
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/protein_id="AAC66075.1"
/db_xref="GI:2690032"
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identified by sequence
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/protein_id="AAC66055.1"
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/db_xref="GI:2690014"
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[TPAPIDENLRKLEAKIIAEEITKLQKTQSSTVVNNFYYNFNGDVLDAEKLVRMLKSK
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Best Local Similarity
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TATGGCTGTGACAAGATTGACAGAAATTATTCCGGTTTACATTTGCTAATAGTTATAAA
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                                                                                       TCCAAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTAC
                                                                                                                       AGGAGGAATACTTTGCATAGCTGGAAATATTCTTGGCCATACAGATGATGAAACAAGAGC
                                                                                                                                                                                            AGGATCCTTTGTCCAAGGAGATTATATTGGTGGTGGCGCAGTGCTTGGATCTCAGTTATT
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5128. .5346
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complement(4623.
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5609. .5707
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WLEYTQKEENQKIKEFANKFIKKRKPKI"
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/product="B. burgdorferi
/protein_id="AAC66200.1"
/db_xref="GI:2690097"
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/product="B. burgdorferi predicted
/protein_id="AAC66199.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGAATAAGC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAATATGGGCCAAGCTAGCGCTCTTGGGTTTGAACTATCTTTCAAAAAAAGTTATTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCAAATCTTAAAAAAAAGACTCGGCATTGATATTGCGGGTTTTGAACCCCAATTTTGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia
AE000786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B. Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidnan,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson,M., van Vugt,\bar{R}., Palmer,N., Adams,M.D., Venter,J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richardson, D., Peterson, J., Kerlayage, A.R., Quackenbush, J., Salzberg, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE000786.1
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic sequence of a Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        burgdorteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE000786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390 (6660),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 29766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 29766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                burgdorferi
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116. .1009
                                                                                                                                                                                                                                                                                    /db_xref="taxon:1
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116. .1009
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                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:2690008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hatch, B., Smith, H.O. and Venter, J
                                                                                                                                                                                                                                                                                                                                                                              .29766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GGATTCCAACTATCGTTTAAAAAAAGATACTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580-586 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spirochaetaceae; Borrelia;
                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp DNA lir
lp28-2, complete
                                                                                                                                                                                            identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid sequence
                                                                                                                                                                                               by Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCT 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19613
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FEATURES
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                                                                                              SdC
                                                                                                                                          gene
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Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
Salzberg,S., Hanson,M., van-Yugt,R., Palmer,N., Adams,M.D.,
Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L.,
Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K.,
Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-DEC-1997) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLSPLEVCCTKIYNLHPNI" complement(1847. .197/gene="BBI03"
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/TYNYVLIQNNENEALAKTYQLKVNYKTLLEYLEILEKNPKVILKRPTNKENESFIGLY
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LTET1FEINLILENYSQKTLLKKYNENLKNKNLPPSNISTMKKYLKQLEKEIKIIAKF
YFKNDQSLLYYKLNYTLEKIWLKLIELFYKELKQFIQKNTTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-
174. .
                                                                   complement(2188.
/gene="BBI05"
                                                                                                                 complement(2188.
/gene="BBI05"
                                                                                                                                                                                                                                                                                                                                                   complement(2124.
/gene="BBI04"
                                                                                                                                                                                                                                                                                                                                                                                                   complement(2124. .2219)
/gene="BBI04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1847. .1972)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BBI02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="BBI02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Borrelia burgdorferi"
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complement(2188. .2310)
                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                    codon_start=1/
                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MVYVLLDFNSLYFGGLALCVWDFYYMVWISILLSEIVSSFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="similar to GP:1655791 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /plasmid="lp28-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBI01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ypothetical protein; identified by
                                                                                            .2310)
                                                                                                                                                                                                                                                                                                                                                                             .2219)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified
                                           identified by Glimmer;
                                                                                                                                                                                                                                                                                                                             identified by
                                                                                                                                                                                                                                 coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ьy
                                                                                                                                                                                                                                                                                                                             Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glimmer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glimmer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.67;
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3911. .4315
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/gene="BBI07"
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SKYKISHIINAGVASGIYSDKNKFIKIGDVVISTETTSYDFDLHRFGYEIGHVPEHPK
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PID:457107 percent identity: 33.62; identified by sequence
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putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYKNIKYSRSLNIGK"
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putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAQVAYGFKIPFIIIRGISDIVNNENNYDDYKKFLKKASSSSAKIVENLIKLM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFKANTALIRKTSKIKINNITSYMGLIITGDQFIDHQTFQEIPEEFENAIAIDMESAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="B. burgdorferi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=1]
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                                                                                                                                                                                                                                                                                                                                    translation="MASEAKIDAEKSNKEVNSQKKSKNNSKNIEVKDTLGLVKAIKKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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Borrelia gas
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AF085741.1
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Bacteria;
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                                                                                                                                                                                                                                                                                                              Noppa, L., varia
                                                                                                                                                                                                                                                                                                                                                                     Noppa,L., Ostberg,Y., Lavrinovicha,M. and Bergstrom,S. P13, an integral membrane profesin of Borrelia burgdorferi,: C-terminally processed and contains surface-exposed domains Infect. Immun. 69 (5), 3323-3334 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi group.
1 (bases 1 to 678)
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pa,L., Ostberg,Y.
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; Spirochaetales; Spirochaetaceae;
                                                                                                              /Codon_start=1
/transl_table=11
/product="membrane protein P13"
/protein_id="abapa8362.1"
/db_xref="GI:4731125"
/translation="MNKFLIFILVIFCAFSSFAQDDSKSTFNLGAGEKFLYYETNKKD
SLYPFILNLFIGFGIGSFAQGDILGGSSILGFDAYDGIGILITGAYLDIKDEDNNAKKA
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177 c 140 g
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121..6
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                                                                                                                                                                                                                                  /chromosome="large linear"
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                                                                                                                                                                                                                                                       /organism="Borrelia garinii"
/strain="Ip90"
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                                          62.9%;
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                                                                        Genomic sequence of a
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Venter,J.C. et al.
                                                                                                                                                 burgdorferi group.
1 (bases 1 to 27323)
                                                                                                                                                                               Borrelia burgdorferi
                                 9403685
                                                                                                                                                                     Bacteria; Spirochaetales;
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 Casjens, S. White, O.,
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  ., Huang, W.M.,
Ketchum, K.A.,
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                                          Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S.,
                               Palmer, N.,
                                                                                                                                           Spirochaetaceae;
disease
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                                Adams, M.D.,
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Sutton, G.G., Clayton, R.A., Dodson, R., Hickey, E.K.,

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RESULT 3
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                                                             AF085739
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AF085739
Borrelia burgdorferi.
Borrelia burgdorferi
Bacteria; Spirochaetales;
                                                   AF085739.1
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 Spirochaetaceae;
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e protein
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655; Conserv
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                                                             AGTTGGTATAGGGTTAATACTTACAGGAGCTTATTTAGATATCAAAGCTCTTGATAAGAA
                                                                                                 TATGAATAAATTTTTAATTGTTGTTTTGCTAGCCTTTTGTGTTTTTTCTAGCTTTGCTCA
           TGCTCCAAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGT
                                                 GGTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTTGGATATCAAAGCGCTTGATGGTAT
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Submitted (24-AUG-1998) Microbiology,
University, Umea S-901 87, Sweden
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1 (bases 1 to 781)

1 (bases 1 to 781)

Noppa,L., Ostberg,Y., Lavrinovicha,M. and Bergstrom,S.

P13, an integral membrane protein of Borrelia burgdorferi,

C-terninally processed and contains surface-exposed domain:

Infect. Immun. 69 (5), 3323-3334 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noppa, L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="membrane protein P13"
/protein_id="AAD28360.1"
/db_xref="G1:4731121"
/translation="MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSK
/DPIVPFLNLFIGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITK
KAAFQWTMGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFD
VAMGQSSALGFELSFKKSY"

3 98 c 153 g 307 t
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122. .661
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/chromosome="large l
122. .661
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/note="similar to
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/strain="B31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
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Pred. No. 1.8e-74;
0; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="signal peptidase I (lepB-1)"
/protein_id="AAC66422.1"
/protein_id="AAC6422.1"
/db_xref="Gi:2689913"
/translation="MAPYLTEEQRLIRKRQRKVFFKYFLTFLILNFFFTKFVLQIFMI
/KSNEMLDTITKNASLFFYATHITSFFIFLKMNDIVLYEDFRKLMFLLTLIKDFFFLN
KIFKRASYKSRIAAVQGDSYYVRGLNVLYNKKDTNFFYLHGNLVSYYKLNDFFNTDE
VIKCFTLKKNEFFLLNNLSVLNDSRIFGPINKNAIVSFLYLKVVDYKIVK"
COMplement (2834. 3814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GFKAPEESDIIIFENPEYKSKGVFFDIFQRILYMLTLSFIDLDRDEYGNPNVRFLVKR
GAFADGKIVRFNNGKAYIKREGEENFILEDSYMDLVDKNFKIKKIVANEDYGIYGDFA
MFVALSQLNINLSSTDDFSFFDVRMIDRFEFERLEYKYLSAFMPYVDYYMEKAIMRDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="signal peptidase I (lepB-2)"
/protein_id="AAC66421.1"
/db_xref="G1:2687912"
/translation="MYLRRLDKFASFLVHIVEKYLTYRKRKKYFCKLRAKKRGFLLNF
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/translation="MYLRRLDKFASFLVHIVEKYLTYRKKYFT"
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/translation="MYLRRLDKFASFLVHIVEKYLTYRKKYFT"
/translation="MYLRRLDKFASFLVHIVEKYLT"
/translation="MYLRRLDKFASFLVHIV"
/translation="MYLRRLDKFASFLVHIV"
/tran
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ENVALEVVDNVDSFILNLADRYSLVITRDIFFAKLLLDLGVKVMNDEGRIFDINNINY
LYFRSKINFNLKIKKKYYDEDFNKSRYEKFITNFYSLFFS"
complement(2197. .2832)
/gene="BB0030"
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TSIRGSSEVLYMTGGYNNLDTKFKVYSNTNNYTTPIFIODEVGEESSYEAREFNDAIL
IGSNNGFAEFTKNKEGIFALRAPSKSVEPGAYNGSQLSKTGLNDIIPVSNNTIYILTQ
GKGLWKLENRKLTKE
                                                                                                                                                                                                                                                                                                                       putative"
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PID:1303831 GB:AL009126 percent identity: 32.58
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/gene="BB0029"
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NILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTYLL
AQNKEEELEVCELNGKDWILKEKKPLKAYKFLKSVGRDGVKEAYILAIDKNNREKIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIYVPDGYILPIGDNRDNSHDGRFFGVINKNKVLGRTLIIYLPFSRVGFI'
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                                                                                              /product="B. burgdorferi predicted coding region BB0032"
/protein_id="AAC66427.1"
/db_xref="GI:2687918"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to PID:1652260 percent identity: 35.98;
identified by sequence similarity; putative"
/codon_start=1
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30.95; identified by sequence similarity; putative"
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/protein_id="AAC66423.1"
/db_xref="GI:2687914"
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/protein_id="AAC66428.1"
/db_xref="GI:2687919"
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IIIPKFKNPGAYLKINSNIENTYIYLNEKYIGRTPLNKYINATEGVLRAKRMGFKTYE
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                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BB0032"
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                                                                                                                                                                                                                                                                                                                                                             /gene="BB0036"
/note="similar to GB:D26185 SP:P05652 GB:X02369 PID:40018
PID:467396 percent identity: 37.98; identified by sequence
                                                                                                                                                                                                                                                                                                                  similarity; putative"
                                                                                                                                    /product="DNA topoisomerase IV (parE)"
/protein_id="AAC66418.1"
                                                                                                                                                                                                                                  transl_table=11/
74.4%;
87.0%;
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complement(8379. .10178)
/gene="BB0036"
complement(8379. .10178)
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="DNA topoisomerase IV (parC)"
/protein_id="AAC66419.1"
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MHDGNFHKVANVVGNTMKYHPHGDTSIYEALVNIANKDLFIEKQGNFGNLFTGDPASA
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5369. .5
                                                                                                                              LEKTFYKTLEGIFTEKKTYKLLETISKEENILSIILSEVLRHKESFSREVLKEDVENL
LKIPTRISLEDIDKNSKDIKLINKELKSINSISSIRGYSINFIDLLLAKYSKEHQR
KTKISLIKSKNVKEIATKNMKVYLNLAEGFAGTSLFDGEFIGNASYYDKILVFRENSY
VLKNIEDKTFIDKKNVCALVYDINNSKEQIFSIIYFNRLDNFYYVKRFKIDKFITDKV
YEFLGENDEFVDFSLNPEFVEFSTNKDIVKRIEIDNFMVKSRSSIGKRISSNNLKKVK
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VIEKLYHYTNCQISISVNLLLLSERYPVVYTIKDLIKFHAAHLQKILKMELELQKSKI
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AKILPHNFNEILNAVKSELLGESYDIYPDFPTGGIVDVNEYADGNGKVLVRAKIETID
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/gene="BB0035"
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QDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(5892. .6431)
/gene="BB0034"
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NNSFASIKKEELHVSKYKEGNIFNHDELFPKLLIKKRELQRLKKFKEKEGYT
LIPISFYLKKSIIKVEGICKGKKLYDKREILKQKSIKKDLSREIKYK"
complement(5892...6431)
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NKENLIKEQLVDENYLKNFNQIGLNEAITGISYFSAIEYANWYSKKLPTGFKARLPIS
QEWELYQKEPNKNPLNINEISKKVGFWNLMQNSSFNEIAIFKNEKNFYSENSNFYSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BB0035"
/note="similar to GP:1405462 percent identity: 31.66;
identified by sequence similarity; putative"
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VAMGQSSALGFELSFKKSY"
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/protein_id="AAC66426.1"
/db_xref="GI:2687917"
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/codon_start=1
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/protein_id="AAC66420.1"
/db_xref="GI:2687911"
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SELKEHPKYIKKFLKDSIPYLNSTEMFKDFLNSYKAIYSIDQDNSNQEEIWNSLKTNF
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Score 641.4; DB 1; Pred. No. 1.1e-86;

Length 14102;

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                                                                                                             CCAAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTACT
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ATGGCTGTGACAAGATTGACAGAAATTATTATTCCGTTTTACATTTGCTAATAGTTATAAT 638
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                       AGGAAACTGAAAAATAGCCTTAATATAGCTTTTGGAGGGTTTGAGCCTAGTTTTGATATT 698
                                                                                                CCAAAAGCCGCTTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAGGTGCAGTTACT
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Direct Submission
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DPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPK
AAFKWTWGKGMMLAGAVTMAVTRLTEIIIPFTFANSYNRKLKNSLNIAFGGFEPSFDI
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/protein_id="AAD28361.1"
/db_xref="GI:4731123"
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/chromosome="large linear"
121. .657
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2 (bases 1 to 14102)
2 (bases ..., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Fraser,C.M., Casjens,S., Ketchum,K.A., Dodson,R., Hickey,E.K., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackehoush,J., Richardson,D., Peterson,J., van-Vugt,R., Palmer,N., Adams,M.D., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
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Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tomb,J.F., Fleischmann,R.D., Richardson,D.,
Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S.,
Hanson,M., van Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.,
Venter,J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
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Location/Qualifiers
                                                                                                    /codon_start=1
/trans1_table=11
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/protein_id="AAC66429.1"
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SVGKIFYSVPITFSINYIFDIGELFQIPVFTNIGFSLMTYGDRNNNITNLRTFDALPT
ISFGSGILMMENYKWAFGATASWWMMFEFGNSAKMAHFALVSLSVTVNVNKL"
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putative"
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                                      /gene="BB0028"
741. .1790
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Borrelia
/db_xref="taxon:139"
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ALIGNMENTS

TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AF085740
noppe, i., Ustreig, i., Lavilnovicha, m. and bergstrom, s. pl3, an integral membrane protein of Borrella burgdorferi, is C-terminally processed and contains surface-exposed domains	burgdorferi group.  1 (bases 1 to 777)	Borrelia afzelii	Borrelia afzelii.		AF085740.1 GI:4731122	AF085740	5	AF085740 777 bp DNA linear BCT 24-APR-2001	

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Title:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result a ၀ ၀ 0000 C No. Score 54.6 54.2 54.2 55 Query Match 114489 33068 3532 307532 307532 307532 3149980 1155932 1153034 1153034 349980 36034 112025 12025 16012 12507 6852 193379 133501 28601 236130 106434 678 52971 29766 27323 173540 18855 53561 7106 Length 73334 73334 18624 60604 73377 DΒ AF0085741 AE000789 AE000789 AE000789 AC119697 AE000789 AC2117080 AX348744 AC221387 AC116956 AX346512 AX346380 ID AF085740 AE001117 Borrelia AF085740 Borrelia AF085741 Borrelia AF085741 Borrelia AF085741 Borrelia AE000786 Borrelia AE000789 Borrelia AE000789 Borrelia AE000789 Borrelia AE000789 Borrelia AC119697 Rattus no AE000789 Sequence AX348744 Sequence AX348744 Sequence AX345512 Sequence AX345512 Sequence AX346380 Sequence AX346380 Sequence AX346380 Sequence AX346384 Sequence AX346386 Sequence AX347027 Sequence AX346386 Sequence AX346380 Sequence AX346380 Sequence AX346394 Sequence AX346394 Sequence AX346394 Sequence AX346395 Dictyoste AC117077 Dictyoste AC117073 Dictyoste AC117073 Dictyoste AC117073 Dictyoste AC117073 Dictyoste AC117073 Dictyoste AC117073 Dictyoste AC117070 Dictyoste AC116918 Dictyoste AC14695 Dictyoste AC16918 Dictyoste AC16918 Dictyoste AX344575 Sequence AX344575 Sequence AX34581 Sequence AX34581 Sequence AX34581 Sequence AX34581 Sequence AX34581 Sequence AX34581 Sequence Description

## ALIGNMENTS

AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AE001117/c
raser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,K., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.F., Fleischmann,R.D., Richardson,D.,	burgdorferi group. 1 (bases 1 to 14102)	Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia	Borrelia burgdorferi	Borrelia burgdorferi.		AE001117.1 GI:2687907	AE001117 AE000783	Borrelia burgdorferi (section 3 of 70) of the complete genome.	AE001117 14102 bp DNA linear BCT 15-DEC-1997	

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser.C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, M., van Vugt, R., Palmer, N., Adams, M.D., Gocayne, J., Venter, J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence of a Lyme disease spirochaete,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390 (6660), 580-586 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 14102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Borrelia burgdorferi"
/db_xref="taxon:139"
95. .733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0027"
95. .733
                                                                                                                                                                                                                                                                                                                       complement(1776. .2207)
/gene="BB0029"
complement(1776. .2207)
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                                                                                                                                                                                                                                                                                                                                                                                                                          LQGSDKTPPQATENDKFYQISNEENLITGNSLKIWQMNNNTYTNIDYQQAKEIMPIIK
TSIRGSSEVLVMTGGYNNLDTKFKVYSNTNNYTTPIFIQDEVGEFSSYFAREFNDAIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0028"
741. .1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIFYNDLSKAYPTNLYPGGIGAIKYQYHILNNLAIGLELRYMFNFDINHSFNILNPDS
SVGKIFYSVPITFSINYIFDIGELFQIPVFTNIGFSLNTYGDRNNNITNLRTFDALPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .14102
                         /translation="MLSKIFYDADSCNFKIIKFLQKFILHNKSKLIVVSNKFFSLEIT
ENVALEVVDNVDSFILNLADRYSLVITRDIFFAKLLLDLGVKVMNDEGRIFDINNINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BB0028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0032"
3885. .5357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BB0033"
5369. .5821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0030"
complement(219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BB0031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BB0030"
                                                                                                  /gene="BB0034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAFADGKIVRFNNGKAYIKREGEENFILEDSYWDLVDKNFKIKKIVANEDYGIYGDFA
MFVALSQLNINLSSTPDFSFFDVRMIDRFEFERLEYKYLSAFMPYVDYYMEKAIMRDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="signal peptidase I (lepB-2),"
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GFKAPEESDIIIFENPEYKSKGVFFDIFQRILYMLTLSFIDLDRDEYGNPNVERLVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2834..3814)
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complement(2834..3814)
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30.95; identified by sequence similarity; putative"
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QRIKIHNKFFGNYSLQINLELVDPEKIIKQRQKELSIMVKIKNINENTKLIPVFSLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to PID:1652260 percent identity: 35.98;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIKCFTLKKNEFFLLNDNLSVLNDSRIFGPINKNAIVSFLVLKVVDYKIVK"
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/note="similar to GP:2073503 percent identity: 47.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSNKIEKIQNYELNSLDSKNISLKSTYNVKEFLIQEQNVTKYEYQDFLKENPKWALN
NKENLIKEQLVDENYLKNFNQIGLNEAITGISYFSAIEYANWYSKKLPTGFKARLPIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLENRAIFWFLENLDKDLKILTKNAPWVKTLAKTLDNENIQLISKNEKINIKLPGFKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELKEHPKYIKKFLKDSIPYLNSTEMFKDFLNSYKAIYSIDQDNSNQEEIWNSLKTNF
/note="hypothetical
putative"
                                                                                                 /gene="BB0034" complement(5892.
                                                                                                                                                                         complement(5892.
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LIPISFYLKKSIIKVEVGICKGKKLYDKREILKQKSIKKDLSREIKYK"
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/protein_id="AAC66420.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEWELYQKEPNKNPLNINEISKKVGFWNLMQNSSFNEIAIFKNEKNFYSENSNFYSLI
                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="hypothetical"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dentified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2197.
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                                protein; identified
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                                       by Glimmer;
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Query Match
Best Local S
Matches 755
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                                               361
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TGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG
                                                                                                                                                                            TTTAATTTTTGTTTTTGGCAACCTTTTGTGTTTTTTCTAGCTTTTGCTCAAGCTAATGATTC
                                                                                                                                                                                                                                                                                                                                                                                       AATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGGTTTTTATGAATAAACT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAATTTCAAGCAATAATTTGAAAAAAGTTAAATTTAAATAACTTTAAAAAACCTTTTTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGTTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAG 60
                                                                                       CGAATTTCAAGCAATAATTTGAAAAAAGTTAAATTTAAATAACTTTAAAAAACCTTTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGTTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAG
                                                                                                                                 GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTT
                                                                                                                                                                                                                                                                        TTTAATTTTTGTTTTTGGCAACCTTTTGTGTTTTTTTTTAGCTTTGCTCAAGCTAATGATTC
                                                                                                                                                                                                                                                                                                                                                                 AATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAACT
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755; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/gene="BB0036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKTIVIRELPFGETTESLISSIEKAIRKNYIKVSSINDFTAENVAIELSLPRGVYASE
VIEKLYHYTNCQISISVNLLLLSERYPVVYTIKDLIKFHAAHLQKILKMELELQKSKI
LEKIFYKTLEQIFIEKKIYKLLETISKEENILSIILSEVLRHKESFSREVLKEDVENL
LKIPIKKISLEDIDKNSKDIKILNKELKSINSNISSIRGYSINFIDLLLAKYSKEHQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MDIRTVLKDNEFLQYSSYVIKDRAIASVVDGFKPVQRRIIHSLFE
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SRYIECRLTPLAFDULYSKEITIYESSYDGRNUEPLLYBKIPVILIQGSGEIAVGNA
AKILPHNENEILNAVKSELLGESYDIYPDFPTGGIVDVNEYADGNGKVLVRAKIETID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Translation="MNKLLIFVLATFCVFSSFAQANDSKNGAFGMSAGEKLLVYETSK 
QDPIVEFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITK 
KAAFQWTWGKOWLAGVYTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFD 
VAMGQSSALGFELSFKKSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:D26185 SP:P05652 GB:X02369 PID:40018 PID:467396 percent identity: 37.98; identified by sequence
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VLKNIEDKTFIDKKNVCALVYDINNSKEQIFSIIYFNRLDNFYYVKRFKIDKFITDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/product="DNA topoisomerase
/protein_id="AAC66419.1"
/db_xref="GI:2687910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(8379. .10178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YEFLGENDEFVDFSLNPEFVEFSTNKDIVKRIEIDNFMVKSRSSIGKRISSNNLKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to GP:1405462 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6499. .8379)
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/protein_id="AAC66426.1"
/db_xref="GI:2687917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="BB0035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="DNA topoisomerase IV (parE)"
/protein_id="AAC66418.1"
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Pred. No. 2.1e-117;
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Borrelia bus
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21189251
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-AUG-1998) Microbiology, University, Umea S-901 87, Sweden
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1 (bases 1 to 781)
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                                VAMGQSSALGFELSFKKSY"
                                                                          /codon_start=1
/trans1_table=11
/product="membrane protein P13"
/protein_id="AAD28360.1"
/protein_id="AAD28360.1"
/db_xref="GI:4731121"
/trans1ation="MMKLLIFYLATFCYFSSFAQANDSKNGAFGMSAGEKLLYYETSK
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122. .661
                                                                                                                                                                                                            /note="similar
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                                                                                                   Borrelia afzelii
Borrelia afzelii
                                                                                burgdorferi
                                                                                         Bacteria;
                     21189251
                                                                   gdorferi group. (bases 1 to 777)
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Pred. No. 5.1e-109;
0; Mismatches 3;
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/strain="ACAI"
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                                                                                          TATGAATAAGTTTTTAATTTTTATTTTTGGTAATCTTTTGTGCTTTTTCTAGTTTTGCTCA
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Borrelia
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Direct Submission
Submitted (24-AUG-1998) Microbiology,
University, Umea S-901 87, Sweden
Location/Qualifiers
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1 (bases 1 to 678)
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                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                 /translation="mnnelifilvifcapsseaQDDSKSTENLGAGEKFLvyeTNKKD SLVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILTGAYLDIKDFDNNAKKA DFKWTWGXGMMLAGVVTWAVFLTEIVLPFTFANNYNRKLKNSLNIALGGFEPSFDIN MGQASALGFGLSFKKSY"

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/protein_id="AAD28362.1"
/db_xref="GI:4731125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Borrelia garinii"
/strain="Ip90"
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                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 52971)
1 (bases 1 to 52971)
1 (bases 1 to 52971)
Casjens,S., Palmer,N., van Vugt,R., Huang,W.M., Stevenson,B.,
Rosa,P., Lathigra,R., Sutton,G., Peterson,J., Dodson,R.J., Haft,D.,
Hickey,E., Gwinn,M., White,O. and Fraser,C.M.
A bacterial genome in flux: the twelve linear and nine circular
extrachromosomal DNAs in an infectious isolate of the Lyme disease
spirochete Borrelia burgdorferi
Mol. Microbiol. 35 (3), 490-516 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE001584
Borrelia
AE001584
                                                                                                                                                                                                                                                                                                 2 (bases 1 to 52971)
Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Lathigra,R., White,O., Dodson,R., Hickey,E.K., Gwinn,M., Peterson,J., van-Yugt,R., Palmer,N., Haft,D., Rosa,P. and Stevenson,B.
                                                                                                                                                                                                                                              Submitted (11-NOV-1999) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   burgdorferi group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi
Bacteria; Spirochaet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyme disease spirochete.
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burgdorferi plasmid
                                                   /note="similar to 67.53; identified
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279. .548
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                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spirochaetales; Spirochaetaceae;
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                                                   GB:U03641 PID:458212 percent by sequence similarity; putat
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1р56,
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hypothetical protein'
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complement(5803. .6339)
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.6330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6336...6674)
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complement(6336...6674)
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Kikeegiinkwieknott"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(5803..6339)
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PID:580906 GB:AL009126 percent identity: 54.17;
by sequence similarity; putative"
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complement(5069, .5830)

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                                                                                                                                                                                                                                                                                  /gene="18012"
6800. -7411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein; identified by Glimmer2; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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/protein_id="AAF07739.;
/db_xref="GI:6382429"
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                                                                                                                                                                                                                                                                                                                                                                                                                          GAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCTT
                                                                                                                                                                                                                                                                                                                GGCATTGCACTTGCGGGGCTTGAACCCAATTTTGACATTGGAAT 4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTAAAAAAAGCTGCTTTTCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAACCGGAGGAGTATTATCAGGAATAGGAGGGCTCACAATTGCAGCATCCTACATCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCACATTAATATTAATTTTAGTTTAACAATGCAAATCTTTGCACAAGAGAAACTTGAA 3652
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Borrella
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                                                                  Borrelia 1
Bacteria;
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                                             burgdorferi
                     gaorieri group. (bases 1 to 29766)
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                                                              burgdorferi
; Spirochaetales;
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                                                                                                                                                                                      burgdorferi plasmid
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                                                                                                                                                  GI:2690008
  Casjens,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.8%;
50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104.8; DB : Pred. No. 8.8e-09
                                                                                                                                                                                                              29766
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Huang, W.M.,
                                                                Spirochaetaceae;
                                                                                                                                                                                                           đđ
                                                                                                                                                                                        lp28-2,
                                                                                                                                                                                                              DNA
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  Sutton, G
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                                                              Borrelia;
                                                                                                                                                                                                         linear
                                                                                                                                                                                      plasmid
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    Clayton, R.
                                                                                                                                                                                                           BCT 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                Borrelia
                                                                                                                                                                                        sequence.
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MEDLINE
PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S., Hanson, M., van-Vugt, R., Palmer, N., Adams, M.D., Gocayne, J.D., Weidman, J., Utterback, T., Watthey, L., McDonald, L., Artiach, P., Bowman, C., Garland, S., Fujii, C., Cotton, M.D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van Vugt,R., Palmer,N., Adams,M.D., Gocayne,J., Venter,J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R.A., Lathlgra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.-F., Fleischmann, R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-DEC-1997) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9403685
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                                          complement(2750.
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complement(2750.
                                                                                                    /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:2239281 percent identity: 63.64; identified by sequence similarity; putative; conserved hypothetical protein, authentic frameshift"
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GVIIRPGYKIMKHILEIQNNIALITTRLSKTDRFSHAFVTSKISELSIIPLGYVFPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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/protein_io=*B.acc66073.1*
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/trans1ation=*MRRSLFITLMGGLMSCNIDSKLSSNKEOKNNNNVKEVSNSVQ
E/KTANS1ATION=*MRRSLFITLMGGLMSCNIDSKLSSNKEOKNANIPNISIVHTQK
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VIEKIHNKKTSLMENYKNNRDKINKLTLLQNNLKINIELEQLINMIDIAENEIRSAAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical
putative"
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116. .1009
                                                                                                                                                                                                                                                                                           IQEDSETPERVKKENFKNKFRHFLDVKYNKKFTAEEILGYIYAILYSNIYRDRFYEHL
QIDFPKIIFVDNSDIFVTLGKLGTDLINSHLVKVVPTININIGKCFSFLDETLKQNSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="BBG02"
1047. 1928
/gene="BBG02"
/note="similar to PIR:A64689 percent identity:
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116. .1009
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1047. .1928
/note="hypothetical protein;
                                                                                                                                                                                                         /gene="BBG03"
                                                                                                                                                                                                                                                    LEKVIKTIHYTIGIQKK"
                                                                                                                                                                                                                                                                        IEKVFYKEETNELYYNQTSRFINVSKEVYNYTIGSWQTLKSYLTYRKGREMPSKEVEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identified by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BBG01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Borrelia
                     /gene="BBG04
                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence similarity;
                                                                                   . 2857)
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  by Glimmer;
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/db_xref="G1:2690031"
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complement(2891. .4056)
/gene="BBG05"
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AKFSKEGNQFKELMLRNAVYNYLEDYDYVIIDTPPSLSSELDNALVIADKVIIPVPLE
RWAVENLPLLINQIKELENNFMGKEAKIIHIFASKVEIGRVTSTEIMSLLKEKYLNKF
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/gene="similar to PID:1174351 percent identity: 39.26;
/note="similar to PID:1174351 percent identity: 39.26;
identified by sequence similarity; putative"
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VGGIEKSYSLSKTYYMEVFFKKGSIFCYFKSLPRILKKENVNTTYNKALFSMETTLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="BBG06"
4208. .5368
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                                                                                                                                                                                                      IGEVHKSEALKKIIDYAIGPKENENYYKEYLRILEKI" 6737. ..7288
                                                                                                                                                                                                                                                                                                                                                        /product="stage 0 sporulation protein J (spoOJ)"
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/db_xref="GI:2690013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BBG08"
5911. .6678
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/note="similar to PID:1143398 PID:1174342 PID:1174350
PID:2182755 percent identify: 57.84; identified by
sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="BBG07"
5378. .5950
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YENYKTKPHFIIENHKYKDLSHIKRKLEKSIERKKENLQKDCENMRTNIFNILIEQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKKVFTFLKKLCIIVNINPIRSSTMINNSKKPNCHNKLQQKLIV
LLSTLAYVNSKYNKYTQKNILZGYLKKINQEPTTTLRTMQNYLYKLEKVFKVTINY
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LVECLNNKNNNIKEERKIIQIEKYQYIKYFNKCNFSLLKEILPILNLDINKDELIKIL
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frameshift"
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVKIDVLKPILKIYLNSKNKLEYNKVFNNNYYYELLEIIKKEKNLQLKEVV"
                                                                                                                          /gene="BBG09"
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TGGTTACTATGGCTGTGACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATA 584
                                                 GAGGCGTTACAGAAAGCACAGCAACAGTAATAACCGGAGGAGTATTATCAGGAATAGGAG
                                                                                                   GTATTACTAAAAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTG
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                                                                                                                                                                                                      ATGCGGTTGGTATAGGGCTTATACTTGCGGGGGGCTTATTTGGATATCAAAGCGCTTGATG
                                                                                                                                                                                                                                                        TAGGGATAGGATCTTTTGTTCAAGGAGATTATATTGGTGGTGGTGCACTACTTGGCTCTC
                                                                                                                                                                                                                                                                                    TTGGAATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTG 404
                                                                                                                                                                                                                                                                                                                                                                                                            TTTATGAAACTAGCAAGCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTAGGGT 344
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2331

2271

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165 TITTTATGAATAAACTTTTAATTTTTTGTTTTGGCAACCTTTTTGTGTTTTTTCTAGCTTTTG 224
CTCAAGCTAATGATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACCTTTTGG 284
                                                                                                                               TTAATATGAAAAAATTTTCACATTAATATTAATTTTTAGTTTAACAATGCAAATCTTTG
                                                                                                                                                                                                                                                                                                                                                       12.2%;
nilarity 52.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(10776. .11015)
/gene="BBG11"
/note="hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTGKAREQALRNLEKTINEKNOKFKDEYSKIFDOLTDENKKILVGVEKSVNEFNNSNY
DFVNEYONLLKEKESREFIIKTLPHTDOVSALOKLNDEINEKNAFVEKYGKSFETL
NESNROVVVALEKOVNEYEKTALDRSFVEAQKALOKEITDLEWETMLLPAKERASSE
KMASSIQAMYKKFVDEHKSQEKKLNEFNRNTIKOLAKALOKEITDLEWETMLLPAKERASSE
KMASSIQAMYKKFVDEHKSQEKKLNEFNRNTIKOYAEKAQDTTKSLYDSMIDGLNVFK
NAFMKDIAGKFLNKDTGESIGEEFHNLINGKDVNWGEGLEKMTTQMYESWKTGLKTAA
GAVFGPWGEAVAELINGLTDFVWGILKGQEKARIKAIEKKRDEDLEELEKRSEVELKK
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PMMIGFEKVKGFLMVALMVPLTKVTTATI YLTTKLGELVAYLAGKWVGGMKMLEKAIT
TPFWKLYEGKLKYVIGKKELATYVSGSFLDREKGAFEPI IKWYGKLLDMISKAYTKKL
NLVTFWKKAEKEKDTSGSEPERDKKFDPNAKTNINKKMAEDYQKLQDEIFNRQRDIYN
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/gene="BBG10"
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/gene="BBG10"
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EIDIIENGIDKTLFNLMKDKKINSKANLITPLRVRLBFQEACDFYKMNPKFANYILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDIETTQLTKTEEAKKLEVERKNKLSKLEPERIKAQAEVDKVNAEDWWNLGKPDRLRK
TQKILDEILKRIAKVKSAGSIEEIKLAHGGARFVSNKPTYMPNSGVMSSEFGQPELVR
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/db_xref="GI:2690014"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TPAPIDENLRKLEAKIIAEEITKLQKTQSSTVVNNFYYNFNGDVLDAEKLVRMLKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                       Score 92.6; DB 1;
Pred. No. 1.1e-06;
D; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 29766;
                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 7
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LOCUS
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MEDLINE
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AE000789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-DEC-1997) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390 (6660), 580-586 (1997)
98065943
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Venter,J.C. et al.
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                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                           /translation="menyQyffnLfflfkIlflyLyIMyKSYKEQQEKGIDHACRILI
LTET1FEINL1LENYSQKTLLKKYNENLKNKNLPPSNISTMKKYLKQLEKEIKIIAKF
YFKNDQSLLYYKLNYTLEKIMLKLIELFYKELKQFIQKNTTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="BBI01"
174. .608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:139"
/plasmid="1p28-4"
174. .608
/note="similar to GP:1655791 percent identity: 66.67;
identified by sequence similarity; putative"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="
                                                                                                                                                                    /gene-"BBI02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ∕organism="Borrelia burgdorferi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                       'gene≖"BBI02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BBI01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ney,L., McDonald,L.,
Cotton,M.D., Horst,K.,
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/trans1_table=11
/product="B. burgdorferi p
/protein_id="AAC66214.1"
/db_xref="GI:2690111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2536
                                                                                                                                                                                                                                                                                                                                                                                                                            KFKANTALIRKTSKIKINNITSYMGLIITGDQFIDHQTFQEIPEEFENAIAIDMESAA
MAQVAYGFKIPFIIIRGISDIVNNENNYDDYKKFLKKASSSSAKIVENLIKLM"
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2536. .3351
                                                             /transl_table=11
/product="B. burgdorferi
/protein_id="AAC66215.1"
/db_xref="GI:2690112"
                                                                                                                                                                                                                                                                                                                               complement(3343.
                                                                                                                                                                                                                                                                                                                                                                                             complement(3343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="pfs protein (pfs)"
/protein_id="AAC66190.1"
/db_xref="GI:2690087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GB:D26562 SP:P24247 GB:M83735
PID:457107 percent identity: 33.62; identified by the control of the cont
   /translation="MQLLKGAIIKLKEDYEKIKKIQNLIKNLIKLH"
3576. .3755
                                                                                                                                                                                                                                                              /note="hypothetical protein;
                                                                                                                                                                                                                                                                                             /gene="BBI07"
                                                                                                                                                                                                                                                                                                                                                          /gene="BBI07"
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/transl_table=11
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PID:473817

predicted

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Glimmer;

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region BBI07"

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/gene="BBI05"
compler:
                               /gene="BBI05"
                                                                                                                                                                                                                                 complement(2124.
/gene="BBI04"
/note="hypothetical protein;
putative"
                                                                                                                                                                                                                                                                                     /translation="MYYVLLDFNSLYEGGLALCVWDFYYMVWISILLSEIVSSFL"
complement(2124. . .2219)
                                                                                                                                                                                                                                                                                                                                                                                                          putative
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TLLSPLEVCCTKIYNLHPNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
/protein_id="AAC66189.1"
/db_xref="GI:2690086"
                                                                                                                                 /codon_start=1
/transl_table=11
/product="B. burgdorferi
/protein_id="AAC66213.1"
                                                                                                                                                                                                   /note="hypothetical protein; putative"
                                                                                                                                                                                                                                                                                                                   /product="B. burgdorferi
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/db_xref="GI:2690109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1847.
                                                                                /translation="MGITIQKFLIKHLGLMRALKPIGESKYFIFY"
complement(2188. .2310)
                                                                                                               /db_xref="GI:2690110"
                                                                                                                                                                                                                                                                     /gene="BBI04"
                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BBI03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BBI03"
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                                                  . 2310)
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Query Match
Best Local Similarity
      Matches
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      325;
    Conservative
                                                                                                                                                                                                                                                                                           /gene="BBI12"
5128. .5346
                                                                                /gene="BBI13"
5609. .5707
                                                                                                                                           /product="B. burgdorferi predicted coding region BBI12"
/protein_id="AAC66200.1"
/db.xref="G1:2690097"
/translation="MIKFPKNHISKIHIIKEYEDVTIKWDREYSLFRKLHGKNKTLED
                                                                                                                                                                                                                                                                                                                                                                                                                                     putative'
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/gene="BBI11"
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/gene="BBI11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mgramtphqqlkvnlenglkminlldellkiaaidgndnniskyndlkkvvdnennqnslikvylknssnedkieakkciktlmhnvetyfesvcdelkdkn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="B. burgdorferi
/protein_id="AAC66198.1"
/db_xref="GI:2690095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              putative'
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3911. .4315
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/protein_id="AAC66197.1"
/db_xref="GI:2690094"
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/protein_id="AAC66196.1"
/db_xref="GI:2690093"
/translation="MIISFEDYNPSASNIFIKITTPKCLKAKLLIPLIQKAQFNNLFS
                                                                                                                                WLEYTQKEENQKIKEFANKFIKKRKPKI"
                                                                                                                                                                                                                                            putative"
                                                                                                                                                                                                                                                        /note="hypothetical
                                                                                                                                                                                                                                                                                                                                                      /product="B. burgdorferi
/protein_id="AAC66199.1"
/db_xref="GI:2690096"
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/gene="BBI10"
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/note="hypothetical protein; identified by Glimmer;
                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                            /gene="BBI12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein;
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                                                                 /gene="BBI13"
                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                       translation="MSKLQGYSTVNYVFPKIQKIKLIYNVKGSVLF"
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                  11.9%;
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Score 90.6; DB 1;
Pred. No. 2.5e-06;
0; Mismatches 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTGGCCATACAGATGATGAAACAAGAGCAACAACTG
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                                                                                                                                                                                                                                                                           1 (bases 1 to 173540)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa;
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Rattus norvegicus clone CH230-135B13,
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AC119697.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Sciurognathi; Muridae;
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Gao,J.,

Garcia, A.,

Garza, N.,

Gill, R.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Worley,K.C.

Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced qi:20467833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (01-MAY-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 173540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorrell,J.H., Guevara,W., Gunaratne,P.,
Harris,C., Harris,K., Hart,M., Havlak,P.
                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases
                                                                                                                                                                                                                                                      Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 113535 bases at least 040
Consensus quality: 119717 bases at least Q30
Consensus quality: 124921 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                Center project Information Center project name: GVPY Center clone name: CH230-135B13
                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.
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MEDLINE
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Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A.,

Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,

Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D.,

Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,

Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (08-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salzberg,S., Hanson,M., van-Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L., Artiach,P., Bowman,C., Garland,S., Fujii,C., Cotton,M.D., Horst,K., Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanson, M., van Vugt, R., Palmer, N., Venter, J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,B.K., Gwinn,M., Dougherty,B., Tomb,J.F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlayage,A.R., Quackenbush,J., Salzberg,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi plasmid lp28-3, complete plasmid \mathtt{AE000784}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9403685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence of a Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Spirochaetales;
burgdorferi group
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                                                                                                                                                                                                                                                                                                                    /gene="BBH02"
391. .858
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                                                                                            /gene="BBH03"
926. .1075
                                                                                                                                     /translation="msrQTNIQFSNEIQALKDTRSTIITNQNDNINSTINYPPYIQTI
LKIEKQVDGNINGMTKESGTETKKLLEILNGNISRFKDAIQYGGSFRAKDVRENQTQK
ENNKDS11H7DDFKEYIHLIMPSINNNADSSSSYYYTNYIINGDNLLRIISNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /plasmid="1p28-3"
273. .467
                                              /note="hypothetical putative"
                                                                                                                                                                                     /transl_table=11
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                     KYSIFKRNSSVKRYTFNHYY"
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/protein_id="AAC65990.1"
/db_xref="GI:2690046"
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identified by sequence similarity; putative"
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              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                   /gene="BBH02"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GP:1655789 percent identity: identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="BBH01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                             'gene="BBH03"
                                                                                                                                                                                                                                                                                                                                                                                    translation="MNKLLIFIILLVFSCNLSNSDQNNPLNMSNKEKISEYQINESSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BBH01"
                                                                                                                           1075
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                                                              protein; identified
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predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                protein'
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coding region BBH03"
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                                                              Glimmer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKKSFLSIYMLISISLLSCDVSRLNQRNINELKIFVEKAKYYSI KLDAIYMECTGAXNDIMTYSEGTFSDQSKVNQAISIFKKDNKTYNKFKELEKKITEEYK PMFLSKLIDDAVDNDVSNARHVADSYKKLRKSVVLAXIESFDVISSKFVDS KFVEASKKFVNKAKEFVEENDLIALECIVKTIGDMVNDREINSRSRYNNFYKKEADFL GAAVELEGAYKAIKQTLL"
                                                                                                                                                                                                                                                                                                                                                                             /note-"This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GB:U03641 PID:458217 percent identity: 63.33; identified by sequence similarity; putative; conserved hypothetical protein, authentic frameshift"
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/transl_table=11
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/db_xref="GI:2690055"
                                                                                                                                                                                                                                         putative
complement(3892.
                                                                                                                                                                                                                                                                                                             complement(3590. .3730)
                                                                                                                                                                                                                                                                                                                                                            complement(3590.
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percent identity: 93.88; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity; putative"
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percent identity: 38.46; identified by sequence
                                                                                                                                                                                                                                                        /note="hypothetical protein; identified by Glimmer;
                                                                                                                                                                                                                                                                                      /gene="BBH08"
                                                                                                                                                                                                                                                                                                                                     /gene="BBH08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2260. .2970)
/gene="BBH06"
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/gene="BBH06"
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/protein_id="AAC65991.1"
/db_xref="GI:2690047"
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/gene="BBH05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1045. .1368
/gene="BBH04"
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1045. .1368
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VTIHY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein; identified by Glimmer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MNSKNRLSSHLITLIYTLNNIDLNSKNIGYYSRGFIRRAFTFNI"
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Best Local
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                                                                                                                                                                                                                                                                             364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                TTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTTACTATGGCTGTGAC 543
                                                                                                                                                                                                                    CCAAGGAGATTATATTGGAGGTGGCTGCACGCTTGGATTTAATTTGCTAGGATTAACCCT 27878
                                                                                                                                                                                                                                                                       TCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGGGCT 423
                                                                                                                                                                                                                                                                                                                                 AGATCTATGGATTCCAGTAATGTTAAATTTATTTTTACCTTTTTGGAGTGGGGTCTTTTGT 27938
                                                                                                                                                             TATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTAAAAAAGCTGC 483
                                                                                                       TTTAACAACTGGAGTTATTCAAATGAAAAATCTGAAAAAAGAACCTGCTAGTATATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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EYEESKYIDNLRIIFSLIKLYSLSFDKSLNIEFSDIAVVISLIENILGNIISSEDNEK
MEKIRKLSSHYKFFHYGIEFPDIQEGFDIVIGNPWEKTKFNEAEFFSKHIFSYRKLS
IKEQNKIKQEILGRDNHPLNIEVNEEKNSMGTINNLYKSDFKNFASGGDDNLFRYFVA
FNLKLIKENGNLTYLVPSALWSESSARILRKYIFTNYKLNYIYQFQNQKRFKDVATLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENNKVNKIATYLKGNIYLTSRSLDRKKSGAYYTPDDLTDFMVISSIEEQLKTKSPLDI
KIIDNSCGSGHFLISCLDYLTEKVWYELDKFEDVKKELDKEYGIILKESEEYDIQDSI
SKELVLKRMLLKRCIYGVDINPISVEITMLSLMINTFIFGTPLSFIEHHIKTGNALLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(8701.
/gene="BBH11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(8000.
/gene="BBH10"
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/gene="BBH10"
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SPIQESIIEFKDSKELILINKMFSKFSTLSEEYINFGVGLNLTKYKTLCKEYNNENFI
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LGYKKIITIFNLLDKGSDAIKFPIFNGGLFAQDKVKYLNNESLLSISEIEEILVKILF
FEEKNIKDKKFVKYSRLDPKSFGELYETLLEYDLRIADTTVHRIVEDGIYLIRTEEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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/protein_id="AAC66002.1"
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NCNFENEKDKNIFLFMLHKLGNV"
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/protein_id="AAC66001.1"
/db_xref="GI:2690057"
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/product="B. burgdorferi predicted coding region BBH09"
/protein_id="AAC66000.1"
/db_xref="GI:2690056"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
on Oct 15, 2001 this sequence version replaced g1:14530013.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr13
RP13-407F1 is from the library RPCI-13.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
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                                                         /clone="RP13-407F1"
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                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                         ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 AATATGCTACCATAGTACCAGTTTTAATAAAAGGGGTTTTTATGAATAAACTTTTAATTTT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 AGCAATAATTTGAAAAAAGTTAAAATTTAAATAACTTTAAAAACCTTTTTTAAATTTCATT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTATGAGATTTTTATGTTGTGATTTTTTTTCACTATAGAACTTTAGATAATTTTAAAAA 75447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             īG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted (31-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GenelD may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,KTunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baumgart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC117080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 106434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium Genome Sequencing Consortium (bases 1 to 106434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deutsche Forschungsgemeinschaft (DFG)
                                                  complement(join(1326. .1349,1442. .1643,1999. 2239. .2246))
                                                                                                                                                                                                                                                                                                                                                    /organism="Dictyostelium
/strain="AX4"
                           /note="ORF_ID:dd_00960
                                                                                                                                                       /pseudo
                                                                                                                                                                                  /note="ORF_ID:dd_00962
                                                                                                                                                                                                                                                      /map="780304-886736"
                                                                                                                                                                                                                                                                                    /db_xref="taxon:44689"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                        1. .106434
                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                         codon_start=1/
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Pred. No. 0.09;
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2 map 780304-886736 strain AX4,
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KDQSLYNLLNQCNTPMGSRLILLQWYKQPLLNAEEIEARINFVEAFYNDLELRQSLRSN
DLKKIGDLBRLSKKLHGQKAFLEDCVHLYGIVTRLPVVLQSLNNHSSHIQGLIKVNFI
ESLESI ISDFAKFCAMVEKT IDLDLANDKHEYVIRSSFDETLRG IQLKKDQ ISNK I ER
FRVDIADDLNILDEAKVKLHYSEKDMFLLRI SRKDEVAI RDKKEY IVHATAKDGVRFAT
REIDTINEAYKKWSAEYLDKODGLAKRTLQI AAASFVPLIEDLSSLIATILDVFVTLSHV
SSIAPI FI RPEI IPLGSDENGAGTVI IGGRHPCVEIQDNVNFI ANDIDLTRGGSQFQ
I ITGRANGGKSTEI RQVGLIVLMAQIGCFVPAQKAT LAVVDCTLSRVGAGDSQLRGVS
TEMALM ETGYSTI IVLATUGI FILDGESCEVAFAGKAT LAVVDCTLSRVGAGDSQLRGVS
TEMALM ETGYSTI IVLATUGI FILDGESCEVAFAGKAT LAVVDCTLSRVGAGDSQLRGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Translation="MENNNDYKNRSTEIFNEADAGFVYQSNSNDYSDGFEGPEKKLDI
RFGPISKGSVKSIAGSPSKVGLRTIDKEKWQTVLDSARCTIISQTSNDHMDSYVLSES
SLFVVERRAMIKTDCGTTTLLHLIAKMYQVGKECGLEVEMVVFSRKNLNQPSKQVPFPHC
SFSDEVNFLNKIFDGQAYVMGDVNKDHWNLYIADFKKNPTLQREGTFFYMHDLDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFMAEMLETSYILKVATKNSLIIIDELGRGTSTYDGFGLAWGIAEYICNQIGGFCLFA
THFHELTILSDLLPMVKNLHVSASTQNNTFTLLYKVEQGPCDQSFGIHVAILANFPSQ
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LDEKKKIEIWSMKPNSKQQWELIKKGSPGNTQMFEDVLLNGNCEGSVMMALKVTREKG
SIVFGISFGDATFKTIGVSQFMDNDNLSNLSSFIMQMSVKECLLCCDQKNYDYQKVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical
/protein_id="AAM45298.1
/db_xref="GI:21281411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(2301. .2392,2533. .2590))
/note="ORF_ID:dd_00996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(9773. .10825
/note="ORF_ID:dd_00992"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYAIQNKTVHGFDGGYDVVVSNYQQLDKKVNFSNDDLIQSIESTNIDLIQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VMKQFFKREGVSAWDTTVNSG1ADLLPGSMIDDFQFDPCGYSMNGLLNEFYWTIHITP
ESHCSYVSFDTNVALADYNQLLAKVLNVFKPGRFTAALYAEDGAPCGDPYTAFDVNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:dd_03346"
/codon start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VIENAKQKAKELESFESNTLKQNHNKFLEEFKEINFNSNDVEKSLSLVNSLLNKYSID
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                                gb|W43468,
                                                                                                                                                                                        FNTGIKSGHWNVIYET"
                                                                                                                                                                                                                                                                                                                  NENSNNEKDENLMI PSRSRLSKELESLGAYLPNEEYTEEVEFDDEEYYEDENDDDNNN
NNNNNEI KEEEKEEEKVENQLNEKGIFI KGGKKFQDMIYRI KENHELSNKHSI DLFND
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/protein_id="AAM45301.1"
/db_xref="G1:21281414"
/translation="MKCFILNNIKRKNIPNNIFKASYSHPSFNNSNNIIRNFSSNNKI
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/protein_id="AAM45300.1"
/db_xref="GI:21281413"
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/protein_id="aam45299.1
/db_xref="GI:21281412"
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/protein_id="AAM45297.1
/db_xref="GI:21281410"
                                                                                                                                                                                                                      KDKLTNHRINGENLVDLFSLYREDPILNNAQFLAKKFNLSEKSVENLLKYTTIPIIVK
                                                                                                                                                                                                                                                          DTHFETPFEITDKQLENNQLIKPNGLSSMISNSDSAFNKVTQSDDISSRISKIKQRIQ
/protein_id="AAM45302.1"
                          /product="unknown protein similar to ESTs emb|Z46294,
pb|W43468, and gb|W43475"
                                                                                                                      /note="ORF_ID:dd_03068"
                                                                                                                                                       join(12150. .12227,12323.
                                                                                                                                                                                                                                                                                 /GEMDSFEETERKVEERLKKKYQEKMETLDSMDQSDFTYKDNEKVDLYNKTSENFTKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation - "MELEKVEKDKLELEVVGDYVFDIPSELISFGNESSWLNINSDKF"
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9.1"
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.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQQQQQQKPQQYQNONOMAYYQQQKLQPQQQQQQQQPPPPY INQQPQQYQQTNSON
NQMNGHANQMNNQMNNQMNNQMGNS IMDGNQMVNNFQQQQQQPQYNPFIDTNLSN
NGLALVPVEQNNNSNNNNNNMMAYYQQQQQQQQQPPPPY INQQPQQQQQQXNSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSQQSIPFIQQAEINQQQQQQQQQFDSNGKPFNPFRDENKYFNSKPQPIESKASFPPF
SEKPFNQHSYLNEKSTMNADQSLGNNSSFYSKIQVQHPTPKSPPTSIYDTQQYKQQQQ
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                                                                                                                                                                                                 SSGSNTLKRLSGRSRSKSYDYDDPFEINPRPLNKSGGYDDYDSFMRKNKRIPGGGSNY
QPKISQQDYYQDNNNNNNNNNNNNYQQQPSSQQIVYHEQSNYNNNNNNNNANRSYNECD
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TSPLRNSGEKKEILTSKDSLSKEFESLSLGNSNNLLNTNQQQQQQQQQQQQQQQPSTQ
join(15592..15843,15949..16261,16362.
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                                                                                              VMGKEMQNHMAYVHNQ"
                                                                                                                                                    YCGKDVGLESMSYHKNTECILRQERCSMCNKLVKHMQMGDHQLQCQTNTYTCGVCGRL
                                                      .16444)
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/codon\_start=1

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SOURCE
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DEFINITION
ACCESSION
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AX251949
BASE CO
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KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAAGCTCTATTGGGAAGCGAATTTCAAGCAATAATTTGAAAAAAGTTAAATTTAAATA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTTGGAATAGGCTCCTTTGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGAT
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                                                                                                                                           Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the Patent: WO 0168911-A 210 20-SEP-2001;
                                                                                                                                                                                                                                                                                                                  Sequence 210 from Patent
AX251949
                                                                                                                                                                                                                                            synthetic construct
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                                                                                                                                Epigenomics AG (DE)
                                                                                                                                                                                                                         artificial sequences.
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GLTVVLNSGDSGAYDLGGPMAANGCERARGDWPSNETYVSAVGZIYFTPYSAPICYD
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/db_xcef="chemically treated genomic DNA (Homo sapiens)"
177 c 1611 g 3193 t
                                                                                           1. .6852
                                                                                                          Location/Qualifiers
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                        AGCAAGCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGG 342
                                                 TTTTTGAATTTCGTAATTATTTAATTTATTTATTAAATTTTTTTGGGAAAAGGATATT
                                                                         GATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAAACT 295
                                                                                                    AAACTTTTAATTTTTGTTTTGGCAACCTTTTGTGTTTTTTCTAGCTTTGCTCAAGCTAAT 235
                                                                                                                                                         TITTAAATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAAT 175
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143; Conserv
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AX348744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequences
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177 c 1611 g 3193 t
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/note="chemic":
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Pred. No. 1.8;
0; Mismatches 144;
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Pred. No. 1.8;
); Mismatches 144;
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RESULT

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                                                                                                                           Submitted (22-JUL-2002) of Molecular and Human (Baylor Plaza, Houston, T
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
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Submitted (04-ApR-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACL16956 133501 bp DNA linear HTC Dictyostelium discoldeum chromosome 2 map 1512060-16455 AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces. ACl16956
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Gloeckner,G., Elchinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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Dictyostelium discoideum
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/chromosome="2"
/map="1512060-1645559"
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AAX30098
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                                                                                              Borrelia burgdorfe
Borrelia afzelii A
Borrelia garinii I
B. burgdorferi ant
B. burgdorferi ant
                                                                                                                                                                                                                                                           Description
                                                   Borrelia
                        Borrelia burgdorfe
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10-SEP-1997;
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Chemically pretrea	AAS45388	22	15732	6.5	49.4	٠.
Human immune syste	ABL33784	24	7461	6.5		
Tumour suppressor	AAS46510	22	12356	6.5	9	_
	ABL32029	24	7351	6.5	9.	
immune sys	ABL33331	24	5518	6.5	9	
Signal transductio	ABK31511	24	47108	6.6	9	Ŭ
chemically	ABN80226	24	19236	6.6	9	_
Signal transductio	ABK31421	24	8992	6.6	9	_
metastasis	ABL34518	24	6381	6.6	0	
	ABL32966	24	6381	6.6	0	•
Chemically treated	ABL70243	24	6381	6.6	50.2	•
0	ABQ66997	24	37515	6.6	0	-
ally t	ABL70604	24	34548	6.6	0	_
	ABL32976	24	18512	6.6	0	
	ABL33345	24	17674	6.7	0	
Signal transductio	ABK31423	24	13123	6.7	0	Ī
Chemically treated	ABL54364	24	13123	6.7	0	_
Human immune syste	ABL33604	24	9084	6.7	0	_
	AAS46787	22	61020	6. 8	۲.	_
Tumour suppressor	AAS46793	22	56153	6.8	۳.	٠.
Human chemically p	ABK40003	24	5586	6.8	۳	•
Human immune syste	ABL32979	24	6963	6.9	52	
	AAX30103	20	74	6.9	52	_
₩.	ABL32299	24	12507	6.9		
l tran	ABK31371	24	6012	6.9	52.2	•
Human gene regulat	AAS61275	24	6012	6.9	2	_
Chemically treated	ABL70328	24	6012	6.9		_
n immune syst	ABL33298	24	12025	6.9	2	_
gene seq	AAX30115	20	396	7.1	ω	
	ABL33702	24	18624	7.1	54	•
Human immune syste	4	24	73334		۸.	•
cally treate	231	24	$\omega$			
n immune syst	347	24	710	٠	4	_
lia burgdorf	025	20	83	7.2	σ	
immune syst	326	24	18855		55.6	
Human gene regulat	AAS61250	24	85	7.5	5	_

## ALIGNMENTS

RESULT 1
AAX30098
ID AAX3
XX AAX3
XX AAX3
XX BOIT
XX B WPI; 1999-215027/18 Borrelia burgdorferi. Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis; ss. Borrelia burgdorferi B31 protein encoding cDNA AAX30098 standard; DNA; 759 (SYMB-) SYMBICOM AB (first entry) 97US-0059036 97DK-0001041 98WO-IB01424 Location/Qualifiers /\*tag= D ВP

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CCCCCCCCCX PX PT X R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a Borrelia burgdorferi B313 protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polycolonal antibody raised against a 13 kDa polypeptide of CC Borrelia burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi CC sensu lato, but is absent from other Borrelia species (e.g. those CC responsible for relapsing fever or avain borrelosis). It should provide CC compared with use of whole bacteria as antigen.
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Best Local S
Matches 759
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                                                                                                           GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTT
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                                                               GACAAGATTAACAGAAAFTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCT
                                                                                                                                                                                                                                                    TGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG
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AAAAAATAGCCTTAATGTAGCTTTAGGAGGATTTGAACCTAGTTTTGATGTTGCAATGGG
                                               GACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCT
                                                                                                                                                                                                                                       TGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTTGGTATAGG
                                                                                                                                                                                                                                                                                                    GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTTGGAATAGGCTCCTT
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Similarity 100.0%;
59; Conservative 0
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Pred. No. 1.8e-145;
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RESULT 2
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                                 The present sequence encodes a Borrelia afzelii ACAI protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC encodes a polypeptide fragment (II) immunologically reactive with CC encodes a polypeptide of Sorrelia burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC to ther spirochaetes. (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such CC infections, in standard immunoassays or amplification/hybridization CC is involved in virulence and is highly conserved within B. burgdorferi cesponsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis,
                                                                                                                                                                                                                                                                                                                    WPI; 199
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                                                                                                                                                                                                                                                     Claim 1; Page 110-111; 118pp; English.
                                                                                                                                                                                                                                                                               Nucleic acid from Borrelia burgdorferi encoding virulence associated protein P13
                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1997;
10-SEP-1997;
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DB; AAY04279.
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                         with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen;
                         use of
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97DK-0001041
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                          whole
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                           antigen.
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Query Match
Best Local Similarity
Matches 671; Conser

78.6%; 88.4%; A;

Score 596.6; Pred. No. 2e-

2e-112;

0

Mismatches

84; 20;

Indels Length

Gaps

2

862; 4.

Sequence

862

вp;

265

94 C;

162

G; 341

T; 0 DB

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RESULT 3
AAX30100
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PN FTT FTT XXX
                                                              Borrelia
                                                                                 Borrelia; P13 antigen;
                                                                                                      Borrelia
                                                                                                                             17-JUN-1999
                                                                                                                                                                    AAX30100 standard; DNA; 749
WO9912960-A2
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                                                                                                      garinii IP90 protein encoding cDNA
                                                             garinii.
                                                                                                                           (first entry)
                            Location/Qualifiers 192..725
                                                                                 spirochaete;
                                                                                                                                                                     ВP
                                                                                  vaccine;
                                                                                 infection;
                                                                                 diagnosis;
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rabbit polyclonal antibody raised against a 13 kDa polypeptide of conters spirochaetes; and/or (ii) hybridizes under stringent conditions to specific nucleic acid sequences but not to genomic DNA from most to specific nucleic acid sequences but not to genomic DNA from most to ther spirochaetes. (I), (II) and transformed cells are useful in vaccines to protect against infection by B. burgdorferi sensu lato. (I), (II) and antibodies raised against (II) are used to diagnose such infections, in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi sensu lato, but is absent from other Borrelia species (e.g. those responsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
Query Match
Best Local Simi
Matches 638;
                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a Borrelia garinii IP90 protein. The present invention describes an isolated nucleic acid (I) that: (i encodes a polypeptide fragment (II) immunologically reactive with
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid from Borrelia burgdorferi encoding virulence associated protein Pl3 \, .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1997;
10-SEP-1997;
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                                                                       Sequence 749 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY04280
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                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            Page 113-114;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0059036.
97DK-0001041.
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                                                                     234 A; 82 C; 150 G; 283 T; 0 other;
                73.5%;
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Score 558.2; DB 20
Pred. No. 1.3e-104;
0; Mismatches 88;
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                                    DB 20;
     88;
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                                  Length 749;
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71.1%;

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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                      This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                     infection caused infection caused for detection
                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999
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                                                                                                                                                                                                                               Page
                                                                                                                                                                                                                                                                       ated Borrelia burgdorferi nucleic acids - us
for the diagnosis, prevention and treatment
y Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                      Erwin AL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENOME SCI INC
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                               275pp; English.
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RESULT 5
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Best Local Similarity
Matches 540; Conserv
                                                                                                                                                          03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
                                                                                     ( HUMA - )
WPI; 1999-189980/16.
P-PSDB; AAY19809.
                                                    Choi GH,
                                                                                                                                          22-JUL-1997;
                                                                                                                                                                                                                                 18-JUN-1998;
                                                                                                                                                                                                                                                                 30-DEC-1998
                                                                                                                                                                                                                                                                                                    W09859071-A1
                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                     Antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX61506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX61506 standard; DNA; 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                                                                                                                                                                                                                                                                                                                                                                                        burgdorferi antigenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAACTAGCAAGCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAGGAAGCTAAAAAATAGCCTTAATGTAGCTTTAGGAGGATTTGAACCTAGTTTTGAT 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTATGGCTGTGACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTAT 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTAAAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGGTATAGGGCTTATACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATT
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                                                                                       MEDIMMUNE INC
                                                                                                       HUMAN GENOME SCI
                                                  Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                        97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                                                                                                                 98WO-US12718
                                                                                                                                                                                                                                                                                                                                                                       vaccine;
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                                                    Hanson
                                                                                                                                                                                                                                                                                                                                                                       Lyme
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Pred. No. 6.3e-101;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      coding sequence,
                                                    Lathigra
                                                                                                                                                                                                                                                                                                                                                                         disease;
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                                                                                                                                                                                                                                                                                                                                                                         infection;
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                                                                                                                                                                                                                                                                                                                                                                         detection;
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RESULT 6
AAX27261
ID AAX
XX AC AAX
AC AAX
XX 04--
DT 04--
XX BOI
KW Ep1
KW ep1
KW 1nf
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OS BOI
XX 9D
OS BOI
XX 9D
OS BOI
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OS 30--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 477;
                                                                               Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme epidemic relapsing fever; endemic relapsing fever; Lyme borrinfection; diagnosis; characterisation; detection; ds.
                                                                                                                                       Borrelia
                                                                                                                                                                 04-MAY-1999
                                                                                                                                                                                            AAX20261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can all be used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                     Borrelia
                                                                                                                                                                                                                      AAX20261 standard;
                                                                                                                                                                                                                                                                                           421
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                                                     burgdorferi
                                                                                                                                  burgdorferi polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 73; 275pp; English.
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                                                                                                                                                              (first-entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 132 A; 62 C; 114 G; 169 T; 0 other;
                                                                                                                                                                                                                      DNA;
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Pred. No. 4.1e-88;
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20-JUN-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-)
                                                                                                       8236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 925-931; 1128pp; English.
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1999-081217/07
                                                                                                                               GGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTAAAAAAAGCTGCTTTTCAATGG
                                                                                                                                                          TATATTGGTGGTGCACTACTTGGCTCTCAAGTGCTTGGAGGAATACTTATAATGGCT
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                                                                             ACTTGGGGTAAGGGAGTTATGTTAGCAGGTGTGGTTACTATGGCTGTGACAAGATTAACA
                                                                                                       GG-----ATACATGACCGGGGATATTGGATTCGTTACAGAAAGCACAGCAACAGTA
                                                                                                                                                                                                                                                                                                                    TTCACATTAATATTAATTTTTAGTTTAACAATGCAAATCTTTGCACAAGAGAAACTTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9399 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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97US-0050359.
97US-0053344.
97US-0053377.
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50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 104.8;
Pred. No. 3.1
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657

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RESULT 7
AAX20310/c
ID AAX20310 standard; DNA; 1:
XX AX20310;
AC AAX20310;
XX DT 04-MAY-1999 (first entry
XX DE Borrelia burgdorferi poly)
XX Borrelia burgdorferi; spii
KW epidemic relapsing fever;
W infection; diagnosis; cha:
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Best Local S
Matches 262
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                           AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrella burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and endemic relapsing fever, and Lyme borrellosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
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                                                                                                                                                                                                                                                                                                                                                                New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayton
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1045-1046; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1998;
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             TTTATGAAACTAGCAAGCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGGT
                                       CTCAAGCTAATGATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGG
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262; Conser
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nilarity 52.1%;
Conservative
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97US-0050359.
97US-0053344.
97US-0053377.
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fever; endemic relapsing fever;
ls; characterisation; detection;
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No. 7.
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7.5e-10;
mes 229;
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fever; Lyme borreliosis;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                    Clayton R,
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                                                                                                                                           OR;
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                                                                                                                                                                                HUMAN GENOME SCI INC
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                                                                                                                                                   Dougherty
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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97US-0050359.
97US-0053344.
97US-0053377.
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prevention
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New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease

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Claim 1;

Page 951-955; 1128pp; English.

AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs

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 RESULT 9
ABL70312
ID ABL7
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DT 01-J
DT Chem
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Cell
KW Cell
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           WO200202807-A2
                              Unidentified
                                                   cancer;
                                                                             Chemically treated cell signalling DNA sequence complementary to#101
                                                                                                   01-JUL-2002
                                                                                                                      ABL70312;
                                                                                                                                          ABL70312 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7074 BP; 3064 A; 906 C;
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                                                  signalling;
er; tumour;
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                                                                                                  (first entry)
                                                 cytosine methylation; cytostatic; ds.
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50.4%;
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Pred. No. 2.3e
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RESULT 10
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         Human gene
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CC The invention relates to a nucleic acid comprising a sequence of at least CR 18 bases of a segment of chemically pretreated DNA of genes associated CR with cell signalling. The activity of the modified sequences of the CR invention may be described as cytostatic. The object of the invention is CR to provide the chemically modified DNA of genes associated with cell CR signalling, as well as oligonuclectides and/or pNA-oligomers for CR detecting cytosine methylations, as well as a method which is CR particularly suitable for the diagnosis and/or therapy of genetic and CR epigenetic parameters of genes associated with cell signalling. The CR chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences CR given in records ABL70111-ABL70626 represent chemically pre-treated CR genomic DNA s of genes associated with cell signalling.

CR Note: The sequence data for this patent is not represented in the printed CR specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genom sequences of genes associated with cell signalling \,
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01-SEP-2000;
  29-JAN-2002
                                                 AAS61250;
                                                                                                  AAS61250 standard;
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                                                                                                                                                                                                                                                      AGCAAGCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGG 342
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                                                                                                                                                                                                                            TGTAAAAAAGTTAATATGTTAAACGTAAAGTTTAAATTATTTTATG
                                                                                                                                                                                                                                                                                                                          GATTCTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                             6852 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; ilarity 49.8%; Conservative
(first entry)
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2000DE-1043826
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                                                                                                  DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG
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Pred. No. 0.
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer. Werner syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilla; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with
1046
                                                                                                                                                                                                                                                                                                                                                                associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                  asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence sequence included in the sequence data for this specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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                                                                                                                                                                                                                                                                            Sequence 6852 BP;
                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 bases of a selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
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                                  176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequences from chemically modified genes associated by gene regulation, useful for analysing cytosine methylations for gnosis and therapy of diseases e.g. severe combined immunodeficien
                                                                                                                                                                       GGAAGCGAATTTCAAGCAATAATTTGAAAAAAGTTAAATTTAAATAACTTTAAAAACCTT 115
                                                                                                                                        2002-017470/02
                                AAACTTTTAATTTTTGTTTTTGGCAACCTTTTTGTGTTTTTTTCTAGCTTTGCTCAAGCTAAT
                                                                                                   TTTTAAATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAAT
                                                                   Similarity
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to 224 nucleic acid sequences comprising chemically pretreated gene associated with gene r
                                                                                                                                                                                                                                                                            1871 A; 177
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                                                                                                                                                                                                         Score 56.6; I
Pred. No. 0.01
0; Mismatches
                                                                                                                                                                                                                                                                            C; 1611 G;
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RESULT 11
ABL32610
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                                                                                                Matches
                                                                                                             Best
                                                                                                                          Query Match
                                          17890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; immune system disease; cytosine methylation;
antiarteriosclerotic; antianaemic; cytostatic: nort
                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer s disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, nevvascular glaucoma and including eye diseases such as retinopathy, nevvascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising for diagnosis and treatm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                                                               Claim 1;
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
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                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurofibromatosis;
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              109
                                                                    49
                                                                                                             Local
AAACCTTTTTTAA-ATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTT
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                                       TTTGTTAAGAAAAAGATTTTTGTTTTATGTTTCGAAAATATGTAAAATTAAAAATTTTTTGAA 17949
                                                                  TCTATTGGGAAGCGAATTTCAAGCAATAATTTGAAAAAGTTAAATTAAATAACTTTAA 108
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                                                      18855
                                                                                                                                                                                                                                                                                                                SEQ ID NO 583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
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2000DE-1043826
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                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                        treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                      5520 A;
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                                                                                                             7.3%;
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                                                                                                                                                                                                                                                                                                                                                       fragment of chemically modified nent of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin
                                                                                                                                                      178 C;
                                                                                                Score 55.6; DB
Pred. No. 0.034;
D; Mismatches 3
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                                                                                                                                                      3950 G;
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                                                                                                                                                                                                                                                                                                                                                                       gene,
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                                                                                                Gaps
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RESULT 12
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrelia burgdorferi; spirochete; bacterium; pathogen; epidemic relapsing fever; endemic relapsing fever; Lyme infection; diagnosis; characterisation; detection; ds.
                                                                                                                     (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia
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       WPI; 1999-081217/07
                                                  White
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a borreliosis;
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RESULT 13
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ID ABL33
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KW antix
KW antix
KW antix
KW antix

Human

immune system associated

gene

SEQ

ij

NO: 1451

immune system disease; cytosine methylation; antiasthmatic;

26-MAR-2002 ABL33478 ABL33478

(first entry)

standard;

DNA; 7106

ВP

antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; a acute myeloid leukaemia; Alzheimer's disease; AIDS; epiler antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;

neurofibromatosis;

rheumatoid

psoriasis;

epilepsy

disease

anaemia;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX20248 to AAX20402 represent polynucleotide sequences Borrelia burgdorferi (Bb). Products derived from Bb can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Borrelia burgdorferi nucleic acids - used t
products for the detection, diagnosis, characterisation,
and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                        TTTGAACCTAGTTTTGATGTTGCAATGGGCCAATCCAGTGCTCTTGGGTTTTGAACTGTCT
                                                                                                                                                                                                                                                            AAAGCGCTTGATGGTATTACTAAAAAAAGCTGCTTTTCAATGGACTTGGGGTAAGGGAGTT
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TAAATTAATAATAGATAATATTTTTATAATCTAATT
                                                                                                                    ACATTCGCAAATCGGCACAATGAAAATCTTAAAAAAAAGACTCAGCGCTGAACTTGCAGGC
                                                                                                                                                ACATTTGCTAATAGTTATAATAGGAAGCTAAAAAATAGCCTTAATGTAGCTTTAGGAGGA
                                                                                                                                                                              ----AGCAAGCATGGTTTTAACATCCTACACAGTTT-----CACTTATTATTCCATTT
                                                                                                                                                                                            ATGTTAGCAGGTGTGGTTACTATGGCTGTGACAAGATTAACAGAAATTATTCTTCCATTT
                                                                                                                                                                                                                                           CGAGAAACACAA - - - - - -
                                                          TTTGAGCCCAATTTTGATCTTGGAATAAACGGATTCCAATTATCGTTTAAAAAAAGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.2%;
50.8%;
                                                                                                                                                                                                                                           -TTAACCGGATACATATTAATAGGGGTAGG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 55;
Pred. No.
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Best Local Similarity
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01-SEP-2000;
6336
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                        GCTTATACTTGCGGGG
                                                  TGTTAGGGTTTTGGGGGGTTTTAGGGTATTTTAAGTTAGTTTTATTGTTTTAGGAAAATA 6335
                                                                           TGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG 420
                                                                                                        GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTT
                                                                                                                                                               GTTGTTAGGTTTTTTAGGATTAAATAAATGATAAAGATTGTGGGGATGGTGTGTGTAT
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                                                                                                                                                                                                                                                                          AATTTGAAAGATTTGGGTTTAAATTTTGTTTTTAATATAATTAGTTTTTGATAAAAATAA
                                                                                                                                                                                                                                                                                                    AATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGGTTTTTATGAATAAACT 180
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2000DE-1043826
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45.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMSZL1, PMSZL12, PMSZL15, PMSZL15, PMSZL16, MGMT, MSSL11, PMSZL11, PMSZL11, PMSZL11, PMSZL12, PMSZL12, PMSZL11, PMSZL13, PMSZL14, PMSZL13, PMSZL14, PMSZL14, PMSZL15, PMSZL16, MGMT, MSSH2, NUTPL1, TREC4, DDIT1L, FANCB, or XRCC8. Nucleic acids of the invention and related cligomers, are useful for diagnosis of diseases associated with gene repair, specifically attain telangiectasia, aging, Bloom's syndrome, cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, immunodefictency, trichthiodystrophy, Fanconi's anaemia, solid tumours and cancer, particularly by determining status of cytosine methylation and/or by deterting single-nucleotide polymorphisms. Determination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair: cytosine methylation; PMS2L1; PMS2L12; PMS2L2; PMS2L3; PMS2L; L4; PMS2L5; PMS2L6; MGMT; MSS2L; NUDT1; TDG; INPPL1; RFC4; DDIT1L; FRACB; ARCCB; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome; Nijmegen breakage syndrome; Werner syndrome; immunodeficiency; trichthiodystrophy; Fanconi's anaemia; solid tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                              chemically pre-treated DNA fragments from genes associated with DNA repair, and their complements.
                                                                                                                                                                                                 and/or by detecting single-nucleotide polymorphisms. Determination of individual methylation patterns may allow development of individualised therapies. The sequences given in records ABL92192-ABL92335 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 128; 25pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid derived from for diagnosis, e.g. of ataxia cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A,
                                                                         Sequence
                                                                                                            European
                                                                                                                             Note: The sequence data for this patent is not represented in the specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2001;
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                    Similarity
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                                                                         73334 BP;
                                                                                                              Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                              Office.
                                                                       24605 A;
                    7.1%;
51.0%;
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                                                                       858 C; 14432 G; 33439
Score 54.2; DB 24; Pred. No. 0.078; 0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes associated with DNA repair, telangiectasia, by determination
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                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryvulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                         01ek
                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-1032529, 01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ
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                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute_myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                     (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurofibromatosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune system disease;
                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                                                                                                                                                              SEQ ID NO 2098; 32pp + Sequence Listing; German.
                                                                                                                                                                                              methylation
                                                                                                                                                                                                                                                                                       Piepenbrock C,
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                                                                                                                                                                                                                                                                                         Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine methylation; antiasthmatic;
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bowel disease;
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24605 A; 858 C; 14432 G;

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                                                                                       AATTTCAAGCAATAATTTGAAAAAGTTAAATTTAA---ATAACTTTAAAAACCTTTTTT 119
                                                                                                                                                                                                                          TTTTGAGATAAATGAAAACGGAAATATAATATTAAATTTTATGGGATAGAGTAAAAAT
AATTCGTGGGTTTAAGGGATTTTTTTTTTTTAGTTTTTTTAGGGGTTGGGATTA 33853
                                                        CTAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTTGGTTTATGAAACTAGCA
                                                                                                           AAATTTCATTAATATGCTACCATAGTACCAGTTTTAATAAAGGGGTTTTTATGAATAAAC
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                                            7.1%;
Similarity 51.0%;
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 Mismatches

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Search completed: March Job time : 269.813 secs 27, 2003, 01:31:20 THIS PAGE BLANK (USPTO)

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Gapop 10.0 , Gapext 1.0
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759
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٠,	CNS00EVL	17	1101	•	ω ·	37
) Tetraodo		17	1184	•	ω.	
_	CNS0075X	17	963	•	ω.	
_	CNS010YV	17	868		w	
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۳	CNS016E2	17	1204	•	ω	
	CNS00HX9	17	1101	7.1	53.8	
~	CNS012FZ	17	1094	7.1	ω	
_	CNS0108N	17	1038	7.1	53.8	
-	B10155	17	809	7.1	54	
T234	AZ045571	17	416	7.1	54	
	CNS00L00	17	1101	•	54.4	
AL060732 Drosophil	CNS001FB	17	1101	7.2	54.6	25
	CNS016RS	17	952		54.8	
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Drosop	CNS0161D	17	1225		55	
AL427102 clone BAO	CNS07360	17	1167	٠	55	21
AL617393 T3 end of	CNS07MAN	17	865	7.2	55	20
вн180441 016_н_20-	BH180441	17	865	•	55	19
AL106578 Drosophil	CNS016C0	17	1200		55.4	18
	CNS015WU	17	1203	•	ū	17
Tetraodo	CNS01U90	17	524	•	ū	16
	CNS0106X	17	1101	7.4	ū	15
Drosophi	CNS016FX	17	1201	•	ப	14
AL071865 Drosophil	CNS00DKY	17	928	7.4	6	13
Tetraodo	CNS01TL7	17	1038		9	12
Drosophi	CNS0182E	17	970		9	11
5414 Drosophi	CNS000D1	17	1101		7	10
064078 Dr	NS0C	17	1101	7.6	7	9
209800	NS020	17	661		58.8	8
5023 Drosophi	CNS0155H	17	1001	7.9		7

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## ALIGNMENTS

REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 1 CNS0039G/c COMMENT DEFINITION ACCESSION Locus TITLE JOURNAL Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefegenoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila. fly), ge AL063921 CNS0039G 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BACC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit Genoscope GSS. AL063921.1 genomic survey sequence. GI:4941778 segref@genoscope.cns.fr

Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                              AAAAAATAGCCTTAATGTAGCTTTAGGAGGATTTGAACCTAGTTTT 646
                                                                                                                                                                                                                                                                                                         GACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCTAATAGTTATAATAGGAAGCT
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                                                                                                                                                                                                                                                                     isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                CNS00LT2 1101 bp
Drosophila melanogaster genome sur
BACR48P19 of RPCI-98 library from
              fly), genomic survey sequence. AL078714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila but provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be constructed.Duffalo.edu/drosophila_bac.htm.
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KKKAATTTTKKKKGKKKKKAAKKKKAADRTKKTKWDAAAAAAAKKTKDKGKKKKKTKK
                                                ACTTGCGGGGGCTTATTTGGATATCAAAGCGCTTGATGGTATTACTAAAAAAGCTGCTTT 486
                                                                                                                                                  AGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTTGGTATAGGGCCTTAT 426
                                                                                                                                                                                                     AAAWTTTDTWAAAWWTTTKKKKKKAAAADKWKDAKKWDGAKKATK-----TKKKDKKA
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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GSS; genome
                                                                                                                                                                                                                               Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 576)
Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetraodontidae; Tetraodon.

1 (bases 1 to 576)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetraodon nigroviridis
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2 (bases 1
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 Conservative
                                                                                   62
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                                                                               /clone="214A06"
/clone_lib="G"
/note="Genoscope sequence ID :
PUC-Or1"
5 c 18 g 444 t
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/clone="71^***
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               42.5%;
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 30;
Score 64.6; DB 17;
Pred. No. 0.012;
0; Mismatches 166;
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                               Length 576;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS00EO7 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope – Centre National de Sequencage :
BP 191 91006 EVRY cedex – FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
                                                                                                                                                                                                                                               found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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                                                                                                       366
                                                                                                 /organism="Drosophila m
/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_11b="RPCI-98"
/note="end : TET3"
a 66 c 104 g 3
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Score 60.6; DB 17;
Pred. No. 0.056;
4; Mismatches 124;
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Query Match Best Local

Matches

109;

Conservative

44;

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Similarity

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                                                                                                     Local
                                        75 TAATTTGAAAAAGTTAAATTTAAATAACTTTAAAAACCTTTTTTAAATTTCATTAATAT 134
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                                                                                  KGAKWTDTRTDDTWKTDTDTWGKADTDWWTDTWKTTWTWTTTTTGWKKWDTKTKTKWKD
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AL098379
AL098379.1 GI:5609990
GSS.
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Drosophila melanogaster genome survey sequence SPO end of an BACM03G04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
                                                                                                                                                                    98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as par Collaboration with the European Drosophila Genome Project (EE http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                    /plasmid="pBeloBAC11"
/note="end : SP6"
108 c 131 g
                                                                                                                                                                                                                                                                                                                             /clone="BACN03G04"
/clone_lib="DrosBAC"
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                                                                         Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
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/organism="Drosophila melanogaster"
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                                                                                                                                           - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BACN13C23 of DrosBAC library from Drosophila melanogaster fly), genomic survey sequence.

AL105073
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Eukaryota; Metazoa; Arthropoda; Hexapoda;
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/note="end : TET3"
66 c 104 g
                                                                             /organism="Drosophila
/db_xref="taxon:7227"
        /plasmid="pBeloBAC11"
/note="end : SP6"
219 c 134 g
                                                  /clone="BACN13C23"
/clone_lib="DrosBAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tetraodon
158P23 of
                                                                      This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                 Submitted (12-APR-2000)
                                                                                                                                                       Direct Submission
                                                                                                                                                                        Genoscope.
                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the
                                                                                                                                                                                                                                                                           Weissenbach,J.
                                                                                                                                                                                                                                                                                       Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                      Human gene number estimate provided Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Saurin, W. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodon nigroviridis
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                                                        http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                freshwater pufferfish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodontidae;
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/organism="Tetraodon nigroviridis"
                                    Location/Qualifiers
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34.58;
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P., Brottier,P.,
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          Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Concer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 150genic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/clone="158P23"
/clone_lib="G"
/note="Genoscope sequence ID
PUC-Ori"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATTTCAAGCAATAATTTGAAAAAAGTTAAAATTTAAATAACTTTAAAAAACCTTTTTTAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAATTTTTGTTTTGGCAACCTTTTGTGTTTTTTTTTTAGCTTTGCTCAAGCTAATGATTCT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214;

    Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as
collaboration with the Berkeley Drosophila Genome Project
The BDGP is constructing a physical map of the Drosophila

                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                 CNS000D1 1101 bp DNA linear GSS 0: Drosophila melanogaster genome survey sequence TET3 end o: BACR01J16 of RPCI-98 library from Drosophila melanogaster
                                                       Submitted (02-JUN-1999) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E
                                                                                                                                                                                                                       ily), genomic survey sequence. AL065414
                                                                                                 Genoscope.
                                                                                    Direct Submission
                                                                                                                                                                                 Drosophila melanogaster.
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/note="end : TET3"
/143 c 100 g
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/organism="Drosophila
/db_xref="taxon:7227"
/db_me="BACRO8E08"
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(E-mail :
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                                                                                                                                                                                                                                                       KWWTRKTWKRDTADWKAWAAWRWRWRRDRKDRRGRRDRWRRWRGADKKWKWDDDDTAKDD
                                                                                                                                                                                                                                                                                                                                                         GGTGTGGTTACTATGGCTGTGACAAGATTAACAGAAATTATTCTTCCATTTACATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKKKTTTTKRAATDKWKWRKKKATAGAWDWDDARRGRGGRWGDKRRRTGARGDKDKTGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WKKTAKKDAGKAAKWKADRTKAWKGAKGAGARGKATAKARAKKRWKDDKDTKKKKTKTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDDKBAKDWKAAADAKAKAAAWHAGTWWTKKDTKKKKKKKKKKGKAKRAATDDTAWTATT
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KGKKKKTKDKDDDDGKRWGRAKAKADAAKAKDDADAADAAWAKAKAKDKDKAKKK
                                               AGCTATTAATTTATTACAAAAATGGGTGATTGCAATTCTGTATTGAAATGG
                                                                                                     DKKKGKDKDRTDDAKATDGKDTWRDTTDTAKRRRKRRRRAGRGRDRKGDKKKRWRARWR
                                                                                                                                                                                                       WTKKDTDWTAGATAGWDDDKAKDGDWKRGTDWRTWKRTWKGWGRKGDKGRKTAGRAGDGK 963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:7227"
/db_aref="AcRO01J16"
/clone="BACRO01J16"
/clone="Lib="RPCI-98"
/clone_lib="RPCI-98"
/note="end: TET3"
104 c 123 g 211 t 383
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18.3%;
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Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN37A19 of DrosBAC library from Drosophila melanogaster (fruit
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Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
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1 (bases 1 to 970)
                                                                                        GSS; genome survey sequence. Tetraodon nigroviridis.
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/note="end : T7"
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/db_xref="taxon:7227"
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This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
Tetracdon nigroviridis DNA sequence
                                                                                                                                                                             Drosophila melanogaster genome BACR27A24 of RPCI-98 library fi
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                                                                          Drosophila melanogaster.
Drosophila melanogaster
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1 (bases 1 to 928)
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/db_xref="taxon:99883"
/clone="194P16"
/clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID : COAG194DH08LP1-end : 152 c 189 g 145 t 186 others
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BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                           GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTT
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/db_xref="taxon:7227"
/clone="BACR27A24"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
fly), genomic survey sequence.
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AL098595.1 GI:5610206
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BACN03K20 of DrosBAC library from
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/note="end : SP6"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Search completed: March 27,

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SUMMARIES

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AF085741 678 bp DNA linear Borrelia garinii membrane protein P13 (p13) gene, AF085741 GI:4731124 Borrelia garinii.

BCT 24-APR-2001 complete cds.

ALIGNMENTS

REFERENCE AUTHORS RESULT 1
AF085741
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM Borrelia garinii
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borreli
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia; Borreli
burgdorferi group.
1 (bases 1 to 678)
1 (bases 1 to 678)
Noppa,L., Ostberg,Y., Lavrinovicha,M. and Bergstrom,S.
Pl3, an integral membrane protein of Borrelia burgdorferi, 1
C-terminally processed and contains surface-exposed domains Borrelia; Borrelia żs

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University, Umea S-901 87, Sweden
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2 (bases 1, Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigras,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F., Fleischmann,R.D., Richardson,D., Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van-'ugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L. Artlach,P., Bowman,C., Garland,S., Fujil.C., Cotton,M.D., Horst Roberts,K., Hatch,B., Smith,H.O. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-DEC-1997) The Institute for Genomic Medical Center Dr, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390 (6660), 98065943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson, M., van Vugt, R., Palmer, N., Venter, J.C. et al. Genomic sequence of a Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathigra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richardson, D., Peterson, J., Kerlavage, A.R., Quackenbush, J., Salzberg, S.,
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section 3
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                                                                                                                                                                                                                                                                                                                    protein;
                                                                  protein;
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                                                                                                                                                                                                                                                   predicted
predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                    identified
                                                                  identified
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                                                                                                                                                                                                                                                                                                                      Glimmer;
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                                                                  Glimmer;
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                                                                                                                                                                                                                                                       BB0027"
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gene

CDS

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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="signal peptidase I (lepB-2)"
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/db_xref="GI:2687912"
/td=Nac6421.1"
/td
                                                   SELKEHPKY IKKFLKDS I PYLNSTEMFKDFLNSYKA I YSI DQDNSNQEE I WNSLKTNF
DLENRA I FWFLENLDKDLK I LTKNA PWVKTLAKTLDNEN I QLI SKNEK I NIKLPGFKK
                                                                                                                                                                QRIKIHNKFFGNYSLQINLELVDPEKIIKQRQKELSIMVKIKNINENTKLIPVFSLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIYVPDGYILPIGDNRDNSHDGRFFGVINKNKVLGRTLIIYLPFSRVGFI"
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MFVALSQLNINLSSTPDFSFFDVRMIDRFEFERLEYKYLSAFMPYVDYYMEKAIMRDY
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/gene="BB0031"
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KSNEMLPTITKNASIEFVATHITSFEIPLKMNDIVLYEDFELSNESTLITLIKDEFETLN
KIEKRASYKYSRIAAVQGDSYYVGLIAVLVNKKOTNEFYLNGNLVSYYKLUDFENTDE
VIKCETLKKNEFELLNDNLSVLNDSRIEGPINKNAIVSFLVLKVVDYKIVK"
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PID:1303831 GB:AL009126 percent identity: 32.58
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1776. .2207)
/gene="BB0029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1776. .2207)
/gene="BB0029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKGLWKLENRKLTKE"
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NILGSSSPRGISLVGETLYIAAMHLFKKENGKIEKIDLSNSYEFINDIVNISGKTYLL
AQNKEEELEVCELNGKDWTLKFKKPLKAYKFLKSVGRDGVKEAYILAIDKNNREKIFD
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30.95; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2197. .2832)
/gene="BB0030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="G1:2687914"
/translation="MLSKIFVDADSCNFKIIKFLQKF1LHNKSKLIVVSNKFFSLEIT
ENVALEVVDNVDSF1LNLADRYSLVITRDIFFAKLLLDLGVKVMNDEGRIFDINNINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSIRGSSEVLVMTGGYNNLDTKFKVYSNTNNYTTPIFIQDEVGEFSSYFAREFNDAIL
IGSNNGFAEFTKNKEGIFALRAPSKSVEPGAYNGSQLSKTGLNDIIPVSNNTIYILTQ
INSNKIEKIQNYELNSLDSKNISLKSTYNVKEFLIQEQNVTKYEYQDFLKENPKWALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical
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identified by sequence similarity; putative"
/codon_start=1
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/protein_id="AAC66422.1"
/db_xref="GI:2687913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2197. .2832)
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/protein_id="AAC66423.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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/db_xref="GI:2687919"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'codon_start=1
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TAGAATTTTCAACAAATAAAGATATTGTTAAAAGAATTGAAATTTGCTAATTTTATGGTTA 60

gene

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Query Match
Best Local S
Matches 659
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                        Similarity
  Conservative
                                                                                                                                                                                       similarity; putative"
                                                                                                                                                                                                             /note="similar to GB:D26185 SP:P05652 GB:X02369 PID:40018
PID:467396 percent identity: 37.98; identified by sequence
                                                                                                                                                                                                                                                            complement(8379.
/gene="BB0036"
                                                                                                                                                                                                                                                                                                           complement(8379.
/gene="BB0036"
                                                                                                                                                                                                                                                                                                                                                                                                         LKIPIRKISLFDIDKNSKDIKILNKELKSINSNISSIRGYSINFIDLLLAKYSKEHQR
KTKISLIKSKNVKEIATKNMKVYLNLAEGFAGTSLFDGEFIGNASYYDKILVFRENSY
VLKNIEDKTFIDKKNVCALVYDINNSKEQIFSIIYFNRLDNFYYVKRFKIDKFITDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKTIVIRELPFGETTESLISSIEKAIRKNYIKVSSINDFTAENVAIELSLPRGVYASE
VIEKLYHYTNCQISISVNLLLLSERYPVVYTIKDLIKFHAAHLQKILKMELELQKSKI
LEKIFYKTLEQIFIEKKIYKLLETISKEENILSIILSEVLRHKESFSREVLKEDVENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHDGNFHKVANVVGNTMKYHPHGDTSIYEALVNIANKDLFIEKQGNFGNLFTGDPASA
SRYIECRLTPLAFDVLYSKEITIYESSYDGRNNEPLLYPAKIPVILIQGSEGIAVGMA
AKILPHNFNEILNAVKSELLGESYDIYPDFPTGGIVDVNEYADGNGKVLVRAKIETID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
/transl_table=16
/product="B. burgdorferi predicted
/protein_id="AAC66426.1"
/db_xref="GI:2687917"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0034"
complement(5892.
/gene="BB0034"
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5369. .5821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="DNA topoisomerase IV (parC)"
/protein_id="AAC66419.1"
/db_xref="GI:2687910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6499. .8379)
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/gene="BB0035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFD
VAMGOSSALGFELSFKKSY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mnkllifyLatfCvfSSFAQAnDSknGafGmSAGEkLLvyETSk
QDPIVPFLLnLfLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="hypothetical protein;
putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="small protein (smpB)"
/protein_id="AAC66420.1"
/db_xref="GI:2687911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKENLIKEQLVDENYLKNFNQIGLNEAITGISYFSAIEYANWYSKKLPTGFKARLPIS
QEWELYQKEPNKNPLNINEISKKVGFWNLMQNSSFNEIAIFKNEKNFYSENSNFYSLI
TEIRTYSQQNNNLLNASTKASFLKNWSSPNIGFRLIVSKE"
                                                                                           /product="DNA topoisomerase IV (parE)"
/protein_id="AAC66418.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GP:1405462 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mntnnlllenkkakfnyfieekisCGIVLkGTEVkSIkakkLSF
NNSFASIKKEELWLENLHVSKYKEGNIFNHDELRPRKLLIKKRELQRLKKFKEKEGYT
                                                                                                                                             /transl_table=11
                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                   YEFLGENDEFVDFSLNPEFVEFSTNKDIVKRIEIDNFMVKSRSSIGKRISSNNLKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MDIRTVLKDNFLQYSSYVIKDRAIASVVDGFKPVQRRIIHSLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPISFYLKKSIIKVEVGICKGKKLYDKREILKQKSIKKDLSREIKYK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GP:2073503 percent identity: 47.68;
identified by sequence similarity; putative"
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            2 (bases 1 to 777)
Noppa, L., Ostberg, Y
Direct Submission
                                                                            Noppa,L., Ostberg,Y., Lavrinovicha,M. and Bergstrom, P13, an integral membrane protein of Borrelia burgdc C-terminally processed and contains surface-exposed infect. Immun. 69 (5), 3323-3334 (2001)
                                                                                                                                                                                                                            AF085740
Borrelia afzelii membrane AF085740
 Submitted
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                                                                                                                                                burgdorferi
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                         Ostberg, Y.
(24-AUG-1998) Microbiology, Medical Microbiology,
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                        Bergstrom,
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/product="membrane protein P13"
/protein_id="AaD28361.1"
/protein_id="AaD28361.1"
/db_xref="G1:4731123"
/translation="MNKELIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKK
/translation="MNKELIVVLLAFCVFSSFAQADDSKSAFNLGAGEKLLAYETSKK
DPIVPFLLNLFLGFGIGSFAQGDILGGFLILGFDAVGIGLILTGAYLDIKALDKNAPK
DAAFKWYNGKGMMLAGAYTMAUTRLTEIIIPFTFANSYNKKLKNSLNIAFGGFEPSFDI
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/chromosome="large line
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D; Mismatches 66;
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                                                                                                                                                       TCTATTGGTAAGCGAATTTCGAGTAACAATTTGAAAAAATTTAAATTAGATACTTCCAA 131
            TGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGG
                                                         AGATGATTCT-----AAAAGCACTTTTAATCTGGGAGCGGGAGAAAAATTTTTGGTTTA
                                                                                                 TATGAATAAACTTTTAATTTTTGTTTTTGGCAACCTTTTGTGTTTTTTCTAGCTTTGCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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1 (bases 1 to 781)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Spirochaetales; Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF085739
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noppa, L., Ostberg, Y. and Bergstrom, S
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                                                                                                                                                                                                                                                                                                                                                     223
                                                                                                                                                                                                                                                                            Conservative
/translation="MNKLLIFVLATFCVESSFAQANDSKNGAFGMSAGEKLLVYETSK
QDPIVPFLLNLFLGFGIGSFAQGDILGGSLILGFDAVGIGLILAGAYLDIKALDGITK
KAAFQWTWGKGVMLAGVVTMAVTRLTEIILPFTFANSYNRKLKNSLNVALGGFEPSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     burgdorferi membrane
                                                                                                                                                                                                                                                                                                                                                                 VAMGQSSALGFELSFKKSY"
                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD28360.1"
/protein_id="AAD28360.1"
/db_xref="GI:4731121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="p13"
/note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-
122. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Borrelia burgdorferi"
/strain="B31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region BB0034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="large linear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
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                                                                                                                                                                                                                                                                                         68.5%;
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                                                                                                                                                                                                                                                                                         Score 513.4; DB 1;
Pred. No. 1.1e-74;
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oded by GenBank Accession
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                                                                                                                                                                                                                                                                             ; 88
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AUTHORS
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MEDLINE
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                                                                                                                                                   Fraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.A., Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K., Gwinn,M., Dougherty,B., Tomb,J.-F.,Fleischmann,R.D., Richardson,D., Peterson,J., Kerlardvage,A.R., Quackenbush,J., Salzberg,S., Hanson,M., van Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.D., Weidman,J., Utterback,T., Watthey,L., McDonald,L. Artiach,P., Bowman,C., Garland,S., Fujil,C., Cotton,M.D., Horst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia
AE000786
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Lathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tombb,J.F., Fleischmann,R.D., Richardson,D.,
Peterson,J., Kerlavage,A.R., Quackenbush,J., Salzberg,S.,
Hanson,M., van Vugt,R., Palmer,N., Adams,M.D., Gocayne,J.,
                                                                                             Submitted (08-DEC-1997) The Institute f Medical Center Dr. Rockville, MD 20850,
                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                          9403685
                                                                                                                                                                                                                                                                                         Nature 390 (6660),
98065943
                                                                                                                                                                                                                                                                                                                     burgdorferi
                                                                                                                                                                                                                                                                                                                                 Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                              Hanson, M., van Vugt, R., Venter, J.C. et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia |
Bacteria;
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                                                                                                                                           Roberts,K.,
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            /organism="Borrelia b
/db_xref="taxon:139"
/plasmid="lp28-2"
116. .1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29766
burgdorferi plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           burgdorferi
                                                                     1. .29766
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spirochaetales; Spirochaetaceae;
                                                                                                                                         Hatch, B., Smith, H.O.
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1p28-2,
                                                     burgdorferi"
                                                                                                                                         and Venter, J.C
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                                                                                                              Genomic
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                                                                                                                                                      hey,L., McDonald,L.,
Cotton,M.D., Horst,
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plasmid sequence
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                                                                                                                                                       Horst, K.,
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/gene="BBG04"
complement(2750.
/gene="BBG04"
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/transl_table=11
/product="B. burgdorferi predicted coding region BBG01"
/protein_id="Aa666073.1"
/protein_id="Aa90030"
/db_xref="G1:2690030"
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/translation="MRKSLFLYTLLMGGLMSCNLDISKLSSNKEQKNNNNVKEVSNSVQ
DGLNDLYSNQEKQKSFTKNFGEWKYEDLINFIEFIFFSESPKNKANIFNISITHTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to GP:2239281 percent identity: 63.64; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQEDSETPERVKKENFKNKFRHFLDVKYNKKFTAEEILGYIYAILYSNIYRDRFYEHL
QIDFPKIIFVDNSDIFVTLGKLGTDLINSHLVKVVPTININIGKCFSFLDETLKQNSI
IEKVFYKEETNELYINQTSRFINVSKEVYNYTIGSWQTLKSYLTYRKGREMPSKEVEH
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1047. .1928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="This region contains an authentic frame shift and is not the result of a sequencing artifact.; similar to GP:2228714 percent identity: 99.12; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity; putative; conserved hypothetical protein,
authentic frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEINLQSKLNNKNNNKLIFFISCSLYLVSTRPFDNRFTYYSKNR
GVIIRPGYKIMKHILEIQNNIALITTRLSKTDRFSHAFVTSKISELSIIPLGYVFPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="conserved hypothetical protein"
/protein_id="AAC66053.1"
/db_xref="GI:2690010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to PIR:A64689 percent identity:
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1047. .1928
/gene="BBG02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="BBG01"
                                                                           /protein_id="AAC66054.1"
/protein_id="AAC66054.1"
/db_xref="GI:2690011"
/translation=""""
                                                                                                                                                                                                                                            /note="similar to
66.76; identified
                                                                                                                                                                                                                                                                                                                          /gene="BBG06"
4208. .5368
                                                                                                                                                                                                                                                                                                                                                                                  4208.
                                                                                                                                                                                                                                                                                                                                                                                                           similarity;
frameshift"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (2891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="B. burgdorferi predicted coding region B/protein_1d="AAC66074.1"
/protein_1d="AAC60031"
/db_xref="Gi:2690031"
/translation="MKQEAISJIFDLEIAVHIKTLDINLNLIYNINGVV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="BBG03"
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/transl_table=11
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YKHLGINFGTEIYYKLNYSKKECYLKINQHFREKKDYRFKARVDNYLNDKFNKNGSVD
LVECLNNKNNNIKEERKIIQIEKYQVIKYFNKCNFSLLKEILPILNLDINKDELIKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
                                                  LLSTLAYVNSKYNKYTQKNILYCFNENLKRNGQPTTTLRTMQNYLYKLEKVFKVTTNY
                                                                                                                                                                                                                                                                                                 /gene="BBG06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                             translation="MKKVFTFLKKLCIIYNINPIRSSTMINNSKKPNCHNKLQQKLIV"
                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                 putative; transposase-like protein, authentic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .4056)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2857)
                                                                                                                                                                                                                                            GB:U03641 PID:458216 per by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identified
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                                                                                                                                                                                                                                                                        percent identity:
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                                                                                                                                                                                                                                            putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region BBG04"
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/gene="BBG07"
5378. .5950
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6737. .7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="stage 0 sporulation protein J (spoOJ)"
/protein_id="AAC66056.1"
/protein_id="AAC66056.1"
/db_xref=="01:2690013"
/translation="MDRKKLAKKPHIIAIASIKGGVGKSTSSIMESTILSKTNKVLLV
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DLDPQNAVTSYFITQOHPRMELINIYNSYSLIKKHKYFKDVVISISKNLDFIPSYLEL
AKFSKEGNOFKELMLANAVYNYLDDVDYDITOTPPSLSSELDNALVIADKVIIFVPLE
RWAVENLPLLINQIKELENNFMGKEAKIIHIFASKVEIGRVTSTEIMSLLKEKYLNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="BBG08"
5911. .6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5911.
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/translation="monmaksqlvkptvrcsnkkdlfikiekdndktivhtkimmdi
ykfgllnkknkukrislrglibkoskvebenlftlraddkflgiyygykrrikkievkyQ
vggieksyslsktyymevrfkkgsifcyfkslprilkkenvnttynkalfsmfttler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIIKRIEINLTKNKNTYLNVSYFKEKONKLKKILSNTOOOLEKNGYNPEQLEISFOKI
YENYKTKPHFIIENHKYKDLSHIKRKLEKSIERKKENLOKDCENMRTNIFNILIEOLK
KEYKIDVLKPILKIYLNSKNKLEYNKVFNNNYYYELLEIIKKEKNLOLKEVV"
                                                                                                                                                                                                       LEKSAKSGSNLEKALNKSSONAIKNFKSLANSVNSVNSKAGSMKSIGKVLKSVGKGLG
SVKNLANKTGEAFNOMLAAFAPIIMAVKAIQAIGSTISGIFDGAMDALDEFNEEVSTF
SDMLGNEDLGKSLAESMRAFGDETLFTRDAIANATKTMLSYGATASEVEERIRWEGEA
AGGSSEGLEKLAEVYSRVESSNOVNLEDLYALRDAGVDITDILAEEAGLAGEALYKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(7483.
/gene="BBG10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7483.
/gene="BBG10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="Myknrkylindrivrnatyintberdkkeyellknelknriedd
irnkintmkilleirnrklyildgykkfedfifdfklartqaykyikiaklifegkle
eidiiengidktlenlmkdkkinskanlitplrvrletqeacdfykmnpkfanyiled
fyqknkeqlikkleyknkokys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6737. .7288
/gene="BBG09"
/note="similar to PID:1143400 percent identity: 43.68;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified by sequence
                                                                                       SDGKTGFDALNKALSKATSEGGKFYGNTAKEAKTLAQAQQQTAKMSEKLFLDIGKALE
PMMTGFEKVKQFLMVAINVPLTKVTTATI YLTTKLGELVALKKWVQGMKMLFKAIT
TPFVKLYEGIKVYLGKLKELATYVSSGFLDRFKGAFEPLIKWVOKLLDMISKAATKLK
NLVTFWKKAEKEKDISGSEPERDKKFDPNAKTNINKKMAEDYQKLQDEIFNRQRDIYN
                                                                                                                                                                                                                                                                                                                              /product="B. burgdorferi predicted coding region BBG10"
/protein_id="AAC66075.1"
/db_xref="GI:2690032"
/translation="MKLDEIIIPLSMSISNNQKLDAIAETLKKIAEQKFSSLDDLKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="conserved hypothetical protein"
/protein_id="AAC66057.1"
/db_xref="GI:2690014"
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/protein_id="AAC66055
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/transl_table=11
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NESNRQVVVALEKQVNEYEKTALDRSFVEAQKALQKETTDLEWETMLLPAKERASAEK
                               KTGKAREQALRNLEKTINEKNQKFKDEYSKIFDQLTDENKKILVGVEKSVNEFNNSNY
DFVNEYQNLLKEKESREREIIKTLPHTDQVSALQKLNDEINEKNKAFVEKYGKSFETL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
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uence similarity; putative"
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55.1"
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                                                                                                                                               ATTTTGACATTGGAAT 2579
                                                                                                                                                                       GTTTTGATATTAACAT 673
                                                                                                                                                                                                                       ATAGATACAACGCAGACCTTAAAAAAAGGCTCGGCATTGCACTTGCGGGGGTTGAACCCA
                                                                                                                                                                                                                                                                                                                    GTGTGGTTACTATGGCTGTGACAAGATTGACAGAAATTGTTCTTCCATTTACATTTTGCTA 597
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                                                                                                                                                                                                                                                                                                                                                                                                                 ATAATAATGCTAAAAAAGCTGATTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTAGGGATAGGATCTTTTGTTCAAGGAGATTATATTGGTGGTGGTGCACTACTTGGCT
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burgdorferi plasmid
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NAFMKDIAGKFLNKDIGES IGEEFHNLI NGKOVWWGEGLEKMITQMYESWKIGLKTAA
GAVFGCWGEAVAELINGLIDEYWGI LKQQEKAE KKAIEKKDEDLEELEKRSEVELKK
LEDRFDEEIKMRKEKLSELDDEYTKEIEFLKQAQSKQI SGEEFQKRLHDVQTEYKTK
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/gene="BBG11"
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/gene="BBG11"
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putative"
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TQKILDEILKRIAKVKSAGSIEEIKLAHGGARFVSNKPTYMPNSGVMSSEFGQPELVR
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Pred. No. 3e-07;
0; Mismatches 331;
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                                              linear
                        plasmid sequence
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Casjens, S., Palmer, N., Van Vugt, R., Huang, W.M., Stevenson, B., Casjens, S., Lathigra, R., Sutton, G., Peterson, J., Dodson, R.J., Haft, Hickey, E., Gwinn, M., White, O. and Fraser, C.M.
A bacterial genome in flux: the twelve linear and nine circular extrachromosomal DNAs in an infectious isolate of the Lyme disease spirochete Borrelia burgdorferi
Mol. Microbiol. 35 (3), 490-516 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Dr, Rockville,
Location/Qualifiers
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856. .1407
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279. .548
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279. .548
                                                                                                                                                                                                                                                        similarity; putative"
                                                                                                                                                                                                                                                                        /note="similar to GB:L31615 GB:L31418 PID:520783 PID:551742 percent identity: 97.81; identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical
putative"
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710. .802
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gylgvhreyvgkigtgllyletegelyvgvlidlirittnkekcn"
                                                                                  TAYQQYLKVKREIERNTINGKIL"
                                                                                                    EQSKDLIKLFGRYKNEQNNKFKSEYYWLYSCISELYSPDIKYSGEEGSPEYDRFMPRP
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IVTEGIfSSLKLYASEHRLLVEIKKTLISLKDPNYRDVPPVRDYNEEYfNKffLDLGS
                                                                                                                                                         /product="outer membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical
/protein_id="AAF07738...
/db_xref="GI:6382428"
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/note="This region contains an authentic frame shift and is not the result of a sequencing artifact; similar to
                                                                                                                                                                                                                   transl_table=11
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                                                                                                                                                                                                                                                                                                                /gene="BBQ03"
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/protein_id="AAF07704.1"
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/db_xref="taxon:139"
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SFVQGDYIGGGALLGSQVLGGILIMAGYMTGDIGFVTESTATVITGGVLSGIGGLTIA
ASYITGIIIPFKFANRYNADLKKRLGIALAGLEPNFDIGINGDSNYRLKNPIEYQFTW
G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(4249. .4986)
/gene="BBQ07"
complement(4249. .4986)
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3623...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="BBQ07"
/note="similar to PID:1143400 percent identity: 62.50;
identified by sequence similarity; putative"
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SEDTPQSKKFRKNTYSPLSAIDVNKLKDLSEIIRNSGQIQGLFNIFNRFGGIFDDSLN
HVYSKKDILGGLEILDLDKLKNSFEKLLSIKETFSKMLNQLLLDYKNDKDHIRTETNK
                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:D26185 SP:P37522 PID:467381
PID:580906 GB:AL009126 percent identity: 54.17;
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene-"BBQ08"
complement(50
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KVLEGAISIDNIKETGFRGLQRQLKENLLNVKKENLSEVNNKKMSIRFFMKNKEFYTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
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identified by sequence similarity; putative"
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                                                                                              complement(5803.
                                                                                                                                             complement(5803.
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NSVKVLINELLEPSVKETYYEETKNTLENIINLHF″
                                                                                                                                                                                                              PQNSLSSYFSKYIFNIDKCNSYSLLKKDVYFGQCINKINDFISIIPSHPILENFNSEI
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                                               /note="similar to
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                      putative"
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GCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAAATTTTTGGTTTAT 305
                                            AGGTAATATTAATATGAAAAAATTTTCACATTAATATTAATTTTTAGTTTAACAATGCAA 3628
                                                                                       GTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTT
                                                                                                                                    CTCCATATATAAAATTTAAAAATTGTGCTAACATTCATTTATAAAAAACTTAATTATTAGG
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6800. .7411
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/gene="BBQ10"
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/gene="BBQ10"
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KIKEEGIINKWIEKNQTL"
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FYTSDSYLGDINNNLLPFSQAYKLASSEIIKLINHFVLTGTVSIQKDGKNQKRLLPNM
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VEAGGEDDLYGICIDIDEFSKTATIVPITNNFEGYLVAKDSTLKVKDKLVFNKDGALE
KVTGAPPNKATINAIALSDAKQISNDVYLIKVAVFGNKAVSKN"
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/db_xref="GI:6382429"
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7418. .8392
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identified by sequence similarity; putative"
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                                                                                                                    Submitted (08-DEC-1997) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
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                                                                                                                                                            Direct Submission
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98065943
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Bacteria; Spirochaetales; Spirochaetaceae; Borrelia;
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/db_xref-"taxon:139"
/plasmid-"1p28-4"
174. 608
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complement(2188.
/gene="BBI05"
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complement(2124.
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PID:457107 percent identity: 33.62; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                            /product="B. burgdorferi predicted coding regi
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TYNYVLIQNNFNEALAKTYQLRVNYKTLLEYLEILEKNPKVILKRPTNKENESFIGLY
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YFKNDQSLIYYKLNYTLEKIMLKLIELFYKELKQFIQKNTTT"
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putative"
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174. .608
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identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                 /note="hypothetical
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/gene="BBI07"
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3576. .3755
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RESULT 8 AC117070

DEFINITION LOCUS

AC117070 Dictyostelium

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AC117070
AC117070.1 GI:20066187
HTG; HTGS_PHASE2.
Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agency: Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 156533)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Noegel, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum
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                                                                                                      VGADIYTGDNCALNTGSGKREVVVPVKFQFEFATLPKVALNFDQIDCTDATNQTRIGV
QPRNITTKGFDCVFYTWNANKVYSLRADYIATALE"
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VGADIYTGDNCALNTGSGKREVVVPYKFQFEFATLLKVALNFDQIDCTDATNQTRIGV
                                                                                                                                                                                                                                                                                                                                                                                        complement(9039. .9800)
/note="ORF_ID:dd_00438"
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/note="ORF_ID:dd_00439"
                                                                                                                                                                                                                                                                                                                                                                                                                                          QPRNITTKGFDCVFYTWNENKVYSLRADYIATALE"
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/note="ORF_ID:dd_00443"
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complement(join(21433.
/note="ORF_ID:dd_00442"
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WPQTVGNLSTVSGECAIDFSSEISVGISDSQWSCLA
WPQTVGNLSTVSGECAIDFSSEISVGISDSQWSCLA
WPQTVGNLSTVSGECAIDFSSEISVGISDSQWSCLA
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EEERKVKAWDIKLKLHLHQETPSKYLTSILKSRAKDKSIFQIKDKDNKTISDKENIAK
RFVEFYQDQYEEKEDNEETHKKLLEKWEVDVDLIKKLEIDRPIRIHEVTKAIKTSSIH
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FTLCQDILDIEKTIISTVNKLSFIKIQRWSMDTLDISKYNRTERIFPNLIGIIAHQLW
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KTIQR"
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DNLNEEQIEEINNMTRWFLFSSVKNTYTEERKYKTMMKIDRAYADWKEGGIKLWDIEL
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ADDIATFTNSTEELMKINTKIQKYCSATSSSLNKEKTVMIAIGDKPHDLPFQESTVPE
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ISNRRPITLLNTDYKILSKILNSRLLDITSKIINKFQNGFVPNRFIQDNIQIMKEVIE
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KTNIDAIKGSKHPIRAFISEYNNKEIRDVRKKKNTSNKNQQPTTTNTTKPIPSTPPTT
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NFIVNGTLNIVRRQKGITVFGRILKEKFTLLHECYSTFKYEDFPLQKFILYTPGYHYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
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FVLETEIQDIDIEDMTQEDNELYTSEETEQDENFDDDDDYYGFDYLDHNDNNINHLMN
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YNSFNSINILLINAPATISERNTFIINSKSLFKKYNSINHQIIAGDFNNNHDCNSFFG
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ITTSNGTKFPIASSIRK"
                                                                                                           IPTPTPIPIIDVELISPLPSPPPPPTTIDNNNKTTPIITPQLIDFDLPSSATILHSPF
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Matches
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Best Local
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                                                                                                             AATAATAATAATAATGAATTTTTATCATTTTTTGATTATTCAAATCCAATTGAAGAT
                                                 AATAAGTTTTTAATTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTTGCTCAAGAT 254
                                                                                                                                                               CCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAAGGGGGTTTTTATG
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FEAKTLEEICFYGCFVCSPIYDFKTYGJTTIRINSTRLSFYSYDFSIFRYLSELIIEE
NIOIQTYFYEKTLPLLK.NLELLEVSKYGEOPFDDUTSPPEKLKTYQFNGISVPLSSIFF
EGVINRIIVKKTLPGFXYFKLTXINTYINTLSLSLNHIDTNVPSMDLFPNLEILNFQI
HNEMSOKGYKNFSIDSINQDWYKRVNAMEIOFINSGKEATIOKFTLOGSLISREKLDY
LLIDGIGFTVDPSIGYLNFSKMTDKGFVHLLFKFVLAGDSGVGKTSILFRITDDTFTE
THITIGIEFKIKTYYIGEKFIKJONDTAGEKRERVHASHYRGCHGVIIVYDVTDQRS
FENVPSMIEDIRRYANENVIKIIIGNKNDLVSOKVVDPFLAQEFADSLDIPFKEISAK
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KTESF INDKLIVDKDKNILYGVGRYVDHYYCVFGKYQLKKSVIKVTKÞDÐNIFISSLDL
LAITNKAYQYMKEQKQMFDYKKTRINISNSÞHGIYRYGINDIHYNGLSTIIEFDTFL
VCSFDVDÞIK"
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EIKNDSQESISKDIIRIIKCNGLSGVUHILLAKLIIKAGKKSKSKOPGSSFITAFLEA
RKIGSLVVLGDRQVGITLQRVWNSLSWLEKIKEVFYLEMASLSEITTEEIDAIKNSSD
ELVNKLLNEFRGRFPSVVHTIVTERDQYMAARLRMCPGKKIVAVVGKGHIGGIIREWE
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/note="ORF_ID:dd_01643"
/codon_start=1
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complement(32023. .32289)
/note="ORF_ID:dd_01641"
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NYknylkedalskkswglesfnqpnqtdddlfketvlleggdntkhvycfidaytanp
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/protein_id="AAM09336.1"
/db_xref="GI:20066222"
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/protein_id="AAM09335.1"
/db_xref="GI:20066221"
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/protein_id="AAM09337.1"
/db_xref="GI:20066223"
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/codon_start=1
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29963. .30505,30619. .30989))
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VGIWGHDLSDLVYNGFSDVLLYKDFIFCEFRVDS"
VGIWGHDLSDLVYNGFSDVLLYKDFIFCEFRVDS"
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/protein_id="AAM09338.1"
/db_xref="GI:20066224"
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Sequence 211 from Patent W00168912
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/db_xref="taxon:32630"
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA
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156; Conserv
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                                                                                                                                                                                                                                                                                                                             artificial sequences
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/db_xref="taxon:32630"
/note="chemically treated genomic
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Olek,A.,
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                                                                                Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with Patent: WO 0176451-A 40 18-OCT-2001;
                                                                                                                                                          synthetic construct. synthetic construct artificial sequences.
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/db_xref="taxon;32630"
/note="chemically treated genom
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Search completed: March 27, 2003, 03:12:31 Job time: 1747.5 secs
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Best Local Similarity 46.9%;
Matches 234; Conservative (
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10185:565 Million cell updates/sec
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immune syst	ABL33156	24	17538	7.4	Ū	45
Human chemically m	ABN80097	24	6169	7.4	٠	44
Tumour suppressor	AAS46370	22	6169	7.4	ū	43
Human DNA for stag	95	24	14147			42
Tumour suppressor	AAS46743	22	14		Ċ	41
Human immune syste	ABL34026	24	59	7.5		40
н	AAS46661	22	02			39
a,	AAS61426	24	19380		ō	38
Human immune syste	ABL34232	24	9021		ġ	37
Human chemically p	ABK40075	24	9021		6	36
Human DNA for stag	ABK33988	24	9021	7.6	56.6	35
immune	ABL33176	24	8077		ġ	34
Human immune syste	ABL32484	24	6244	7.6	ō	$\omega$
r suppresso	AAS46336	22	7348	7.6		32
Human immune syste	ABL34330	24	4163	7.6		31
Human metastasis a	ABL34556	24	13125	7.6	7.	30
Human immune syste	ABL33226	24	13125	7.6	7.	29
Chemically treated	ABL70283	24	13125	7.6		28
æ	ABL33169	24	7781	• -	7.	27
Human immune syste	ABL32184	24	15387	7.7		26
The second	AAS46802	22	8237	7.8	œ	25
immune	ABL32990	24	9731			24
Human immune syste	ABL32515	24	6464		5	23
Human immune syste	ABL33276	24	5675			22
Human anglogenesis	ABQ67089	24	3873			21
immune syst	ABL33421	24	9707		0	20
Human immune syste	ABL34105	24	14023		1.	19
ption	ABK28137	24	6391		2	18
immune	ABL32891	24	6131		Ü	17
Human immune syste	ABL32476	24	14095		Ü	16
O	AAS63345	24	7479			15
	ABK40058	24	44		ω ·	14
	ABQ67059	24	34688			13
	129	24	7110			12
_	L335	24	7110	8.8	66	11
Chemically treated	ABL70587	24	7110			10

## ALIGNMENTS

RESULT 1 AAX30100

AAX30100 standard; DNA; 749

ВP

Borrelia garinii IP90 protein encoding cDNA

17-JUN-1999 AAX30100;

(first entry)

CDS WPI; 1999-215027/18 04-SEP-1998; Borrelia garinii. Bergstroem S; 16-SEP-1997; 10-SEP-1997; 18-MAR-1999 W09912960-A2 Borrelia; P13 antigen; spirochaete; vaccine; infection; diagnosis; ss. (SYMB-) SYMBICOM AB 97US-0059036 97DK-0001041 98WO-IB01424 Location/Qualifiers 192..725 /\*tag= a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The present sequence encodes a Borrelia garinii IP90 protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polyclonal antibody raised against a 13 kDa polypeptide of CC Borrelia burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC to ther spirochaetes. (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such in standard immunoassays or amplification/hybridization tests. (I) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi Sensu lato, but is absent from other Borrelia species (e.g. those cresponsible for relapsing fever or avain borrelosis). It should provide a more specific and sensitive antibody response, and diagnosis, compared with use of whole bacteria as antigen.
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                                                                                                         TCGGGATAGGTTCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTG
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                                               TGGTTACTATGGCTGTGACAAGATTGACAGAAATTGTTCTTCCATTTACATTTGCTAATA
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                    The present sequence encodes a Borrelia afzelii ACAI protein. The CC present invention describes an isolated nucleic acid (I) that: (i) CC encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polyclonal antibody raised against a 13 KDa polypeptide of CC Borrelia burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC to ther spirochaetes. (I), (II) and transformed cells are useful in CC vaccines to protect against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such CC infections, in standard immunoassays or amplification/hybridization CC tests. (I) are also used to produce recombinant (II). The 13 kD protein CC is involved in virulence and is highly conserved within B. burgdorferi CC sensu lato, but is absent from other Borrelia species (e.g. those CC responsible for relapsing fever or avain borrelosis). It should provide CC a more specific and sensitive antibody response, and diagnosis, CC compared with use of whole bacteria as antigen.
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P-PSDB; AAY04279.
Sequence
                                                                                                                                                                                                                                                                                                                    Nucleic acid from Borrelia burgdorferi encoding virulence associated protein P13
                                                                                                                                                                                                                                                                                                                                                                                                       Bergstroem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9912960-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia afzelii ACAI protein encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX30099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX30099
                                                                                                                                                                                                                                                                                                                                                                                                                                   (SYMB-) SYMBICOM AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1997;
10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTATAACAGGAAGCTGAAAAATAGTCTTAATATAGCCTTGGGAAGGATTTGAGCCTAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P13
 ВP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0059036.
97DK-0001041.
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  265
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Query Match
Best Local Similarity
Matches 673; Conser

Conservative

81.0%; 90.1%;

Score 607; DB 20; Pred. No. 3e-107; 0; Mismatches 70;

Length

862; 4;

Gaps

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                                                                                                                              Borrelia
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                                                                                                                                                                                                                                                                                                   AAX30098;
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                                                                                                                                                                                                            burgdorferi B31 protein encoding cDNA.
                                                                                                                              burgdorferi.
                                                                                                                                                                    P13 antigen;
                                                                                                                                                                                                                                                      (first entry)
                                                              Location/Qualifiers 170..709
                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                      spirochaete;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC present invention describes an isolated nucleic acid (1) that: (1) ce encodes a polypeptide fragment (II) immunologically reactive with CC rabbit polyclonal antibody raised against a 13 kDa polypeptide of CC Borrella burgdorferi B313, but not reactive with most proteins from CC other spirochaetes; and/or (ii) hybridizes under stringent conditions CC to specific nucleic acid sequences but not to genomic DNA from most CC to specific nucleic acid sequences but not to genomic DNA from most CC to specific nucleic against infection by B. burgdorferi sensu lato. CC (I), (II) and antibodies raised against (II) are used to diagnose such CC (I), (II) and antibodies raised against (II) are used to diagnose such CC (I), (II) are also used to produce recombinant (II). The 13 kD protein is involved in virulence and is highly conserved within B. burgdorferi CC sensu lato, but is absent from other Borrella species (e.g. those CC a more specific and sensitive antibody response, and diagnosis, CC compared with use of whole bacteria as antigen.
                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a Borrelia
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P-PSDB; AAY04278.
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10-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 759
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                                                                                                                                                                  ATTGTTAAAAGAATTGAAATTGATAATTTTATGGTCAAATCAAGAAGCTCTATTGGGAAG
             TGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG
                                                       GCAAGATCCTATTGTACCATTTTTATTGAACCTTTTTTTAGGGTTTGGAATAGGCTCCTT
                                                                     GAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGGGATAGGTTCTTT
                                                                                                              TAAAAATGGTGCGTTTGGGATGAGTGCTGGAGAAAAACTTTTGGTTTATGAAACTAGCAA
                                                                                                                          ----AAAAGCACTTTTAATCTGGGAGCGGAGAAAATTTTTTGGTTTATGAAACTAATAA
                                                                                                                                                                                                                                                                                  CGAATTTCAAGCAATAATTTGAAAAAAGTTAAATTTAAATAACTTTAAAAAACCTTTTTTA
 TGCTCAAGGAGATATTCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAGG
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 228 A; 90 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0059036
97DK-0001041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borrelia burgdorferi encoding virulence associated
                                                                                                                                                                                                                                                                                                                                                                                                            74.5%;
                                                                                                                                                                                                                                                                                                                                                                                          Score 558.2; Ub ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 G; 284 T; 0 other;
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ID AAXX61505
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20-JUN-1997;
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                                         This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                 New isolated Borrelia burgdorferi nucleic acids - used products for the diagnosis, prevention and treatment of caused by Borrelia, particularly Lyme disease
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MEDIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwin AL,
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97US-0050359.
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Best Local S
Matches 462
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                  (HUMA-)
                                                                                                                                                                                                                                                                                       AAX61506;
P-PSDB; AAY19809
         WPI; 1999-189980/16.
                              Choi GH,
                                                                                                                                      18-JUN-1998;
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                                                                                                                                                                                                    Borrelia burgdorferi
                                                                                                                                                                                                                         Antigenic protein;
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462; Conserv
                                                   MEDIMMUNE
                                                             HUMAN
                              Erwin AL,
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                                                                                                                                                                                                                                                                  (first entry)
                                                             GENOME SCI INC
                                                                                 97US-0057483.
97US-0050359.
97US-0053344.
97US-0053377.
                                                                                                                                      98WO-US12718
                                                    INC
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Pred. No. 3.1e-68;
); Mismatches 72
                                                                                                                                                                                                                          disease;
                              Lathigra
                                                                                                                                                                                                                           infection; detection;
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RESULT 6
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Matches 4
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Best Local S
                                                                          Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme epidemic relapsing fever; endemic relapsing fever; Lyme borr infection; diagnosis; characterisation; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can all be used for detection of members of the Borrelia genus.
                                                                                                                             Borrelia burgdorferi polynucleotide sequence
                                                                                                                                                          04-MAY-1999
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409; Conserv
                                                   burgdorferi
                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                           DNA; 1761 BP
                                                                                                                                                       entry)
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Pred. No. 9.7e
0; Mismatches
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borreliosis;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borrellosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Borrelia burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation, and therapy of infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ( HUMA - )
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                                                                                                                       GGTTCGGGATAGGTTCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTTCTTATTCTTGGAT
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                        ATAATAATGCTAAAAAAGCTGATTTTAAGTGGACTTGGGGTAAGGGAATGATGTTGGCAG
                                                                 TTGATGCGGTTGGTATAGGGTTAATACTTACAGGAGCTTATTTGGACATCAAGGATTTTG
                                                                                                         CTTTAGGGATAGGATCTTTTGTTCAAGGAGATTATATTGGTGGTGGTGCACTACTTGGCT
                                                                                                                                                                                        TGGTTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTAG
                                                                                                                                                                                                                                   CTAGTTTTGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAAATTTT
                                                                                                                                                                                                                                                                         GAGGTAATATTAATATGAAAAAATTTTCACATTAATATTAATTTTTAGTTTAACAATGC
                                                                                                                                                                                                                                                                                                 AAGG----GGTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTT
                                                                                                                                                                                                                                                                                                                                                        AATAGTTCCAAAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATA
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                                                 CTCAAGTGCTTGGAAGG-----AATACTTATAATGGCTGGACACATGATCGTAGGAGGTA
                                                                                                                                                              TGAAATATGAAAGCGAAAAAGCAACCATACTAGCACCATTACTTTTGAATATCTTTTTGT
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336; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraser
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Pred. No. 5.2e
0; Mismatches
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                                                                               Query Match
Best Local S
Matches 324
                                                                                                                                                                                                                                                     AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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epidemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 925-931; 1128pp; English.
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ACAAATAAAGATATTGTTAAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGC
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                                                                                                       Similarity
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relapsing fever; endemic
n; diagnosis; characterisa
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                                                                               Conservative
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                                                                                                                                                                                  BP;
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97US-0050359.
97US-0053344.
97US-0053377.
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                                                                                                                                                                                  3470 A; 1281 C;
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                                                                                                  12.2%;
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                                                                                                     Score 91.6;
Pred. No. 1.
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                                                                             Mismatches
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relapsing fever; Lyme borreliosis;
ation; detection; ds.
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                                                                                                       DB 20;
                                                                                                                                                                                  3595 T;
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Borrelia burgdorferi; spirochete; bacterium; pathogen; I epidemic relapsing fever; endemic relapsing fever; Lyme infection; diagnosis; characterisation; detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi polynucleotide
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97US-0050359.
97US-0053344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrella burgdorferi (BD). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacteria called Spirochetes to a repathogenic in humans and Borrelia causes epidemic and
                                                                                                                                                                                                                             3339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 951-955; 1128pp; English.
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                                                             GGCTGTGACAAGATTGACAGAAATTGTTCCTTCCATTTACATTTTGCTAATAATTATAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 3064 A; 906 C; 866 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infections, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis, characterisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 82.2;
Pred. No. 7
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06-APR-2000;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequen (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation st and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with Cpc dinucleotides e.g. cancers and tumours. The probes can also be used in a method for
                                                                  Note: The sequence value of the printed specification, of the printed specification, of the directly from WIPO at format directly from WIPO at
                                                                                                                                                                                                 differences serving as basis for diagnosis and/or prognosis events are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                         diseases, by analysing cytosine methylations. The parameters may compared to another set of genetic and/or epigenetic parameters,
                                                                                                                                                                                                                                                                                                                                               ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
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01-SEP-2000;
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
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                                                                                                                                                 The sequence data for this patent did not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
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; 2000DE-1019058.
; 2000DE-1019173.
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; 2000DE-1043826.
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or pNA-oligomers for detecting cytosine methylations, as well as a method which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01ek
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                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genom sequences of genes associated with cell signalling \,\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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01-SEP-2000;
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Note: The sequence data for this patent is not represented in the printed specification, but is based on sequence information supplied by the
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                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                  2000DE-1032529
2000DE-1043826
                                                                      2001WO-EP07537
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                                                                                  cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Precelampsia; can allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, can be used in the diagnosis and treatment of immune system disorders, can be used in the diagnosis and treatment of immune system disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     156;
                                                                                                                                                                                                           gene regulation-associated gene oligonucleotide #245
                                                                                                                                                                            Gene regulation-associated gene; severe combined immunodeficiency;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1529; 32pp + Sequence Listing; German
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Best Local Similarity
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                       TAACAATTTGAAAAAAGTTAAATTTAAATAGTTCCAAAAGCCTTTTTTAAATTTCATTAA 154
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                                                                        Piepenbrock C,
               1977
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease.

Note: The sequence data for this patent did not form part of the printed at the point of the printed at the patent of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the printed at the patent did not form part of the patent did not form patent did n
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inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds;
macular degeneration; inflammatory bowel disease; Crohn's disease;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34688
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TTTGGTAATCTTTTGTGCTTTTTCTAGTTTTTGCTCAAGATGATTCTAAAAGCACTTTTAA
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                                                                                                                                                                                                                                                                                                                                                         Score 66; DB -
Pred. No. 0.001;
Pred. No. 150;
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                                                                                                 The invention relates to a nucleic acid comprising a sequence at CC least 18 bases in length of a segment of the chemically pretreated DNA CC of genes associated with pharmacogenomics according to one of the Cs sequences of the genes ALDHG (NM_000693), CYP11A (NM_000781), CYP11B1 (CC (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2 (NM_001979), OCLN (NM_002538), TXNRDI (NM_003330), UGT8 (NM_003360), CC (NM_001979), OCLN (NM_001990), NM_019901, NM_019902, NM_019898, CC (NM_01989) and their complementary sequences, or a sequence (S1) chosen CC from 87 sequences and their complements. The chemical pretreatment CC is bisulphite treatment to convert cytosines (but not methyl-cytosines) CC into uracils. Also included are an ollowmer (II) in particular an CC oligonuclectide or a peptide nucleic acid (PNA)-oligomer, comprising in CC convert least one base sequence having a length of 9 nucleotides CC which hybridises to or is identical to a chemically pretreated DNA of CC genes associated with pharmacogenomics and their complements, arranged in CC conformation of the S7 sequences. The oligomers may also be used as PCR primers. CC The set of 87 nucleic acids and their complements is useful for diagnosis cand therrary of solid tumours and complements is useful for diagnosis of the Harman of soliders and their complements.
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               and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer -
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01-SEP-2000;
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chemically pretreated gene sequence #70 strand
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           06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                        solid tumour; cancer; cytosine methylation; epigenetic; eye; kidne single nucleotide polymorphism detection; SNP; stool; urine; lung; cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
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                                                                    06-APR-2001;
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                                                                                                                 WO200176451-A2
                                                                                                                                                                                               solid tumour;
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Pred. No. 0.0024;
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New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumour and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism

Claim 1; Page 109-111; 143pp; English.

The invention relates to a nucleic acid (I) comprising a sequence at CC least 18 bases of a segment of the chemically pretreated DNA of genes cassociated with metabolism such as DUSP2 (NM\_00418), EPHX2 (NM\_001979), CC QDPR (NM\_00320), SGSH (NM\_000199), SHMT2 (NM\_005412), SLC7A2 (CC (NM\_003046), SLC7A4 (NM\_000199), SHMT2 (NM\_001071) (all cundefined). (I) are useful for diagnosis and therapy of metabolic CC disease, solid tumours and cancers; as primer oligonucleotides for the camplification of DNA sequences, for detecting the cytosine methylation CC state and/or single nucleotide polymorphisms (SNPs) in a chemically treated DNA of genes associated with metabolism. An array of (I) is CC useful for ascertaining genetic and/or epigenetic parameters for the CC diagnosis and/or therapy of existing diseases or the predisposition to CC specific diseases by analysing cytosine methylations. The method involves CC chemically treating genomic DNA sample by a solution of bisulphite, CC unmethylated at the 5th-position are converted to uracil or another base CC which is dissimilar to cytosine in terms of hybridisation behaviour and CC amplifying fragments of the chemically pretreated genomic DNA. The converted of DNA comprising, for e.g. cell lines, biopsies, blood, sputum, CC sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum, CC stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast converted as a converted to combinations. Genetic CC parameters are mutations. In particular insertions, deletions, boint parameters are mutations, in particular insertions, deletions, poi mutations, inversions and polymorphisms of genes associated with metabolism and sequences further required for their regulation. Epigenetic parameters are in particular cytosine methylations and further chemical modifications of DNA bases of genes associated wi metabolism. Further epigenetic parameters include for e.g. the acetylation of histones which correlates with DNA methylation. AAS63306-AAS63373 represent chemically pretreated metabolism associated

Sequence 7479 BP; 2133 A; 68 C; 1273 G; 4005 T; 0 other

and related primers

of

the invention.

Matches Query Match Local Similarity Conservative 8.5%; 46.9%; Score 63.8; Db 24, Pred. No. 0.0024; ""amatches 262; Indels Length ω •• Gaps ;;

- 밁 Š 17 TAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGCTCTAT TGAATATTTTTTTTTTAGTTATTTTTTTTTAGTTTTGTTTTATGTTTAGTTTAGTTTT 6428 76
- Qy 밁 6429 TGGTAAGCGAATTTCGAGTAACAATTTGAAAAAAGTTAAATTTAAATAGTTCCAAAAGCC
- δÃ TTTTTTAAATTTCATTA---ATATGCTACCATAATACCAGTTTAATAAAGGGGTTTTTAT 193
- δõ 밁 194 GAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTTGCTCAAGA 6548
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Post-processing: Minimum Match 0%
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 Drosophila
               CNS00EO7
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/db_xref="taxon:7227"
/clone="BARCR48P19"
/clone_lib="RPCI-98"
/note="end : TET3"
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Matches 146;
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131 AAAGCCTTTTTTAAATTTCATTAATATGCTACCATAATACCAGTTTAATAAAAGGGGTTTT 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AACAAATAAAGATATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAG 70
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                                                                                                                                                                                                                                                                                                                    TAATWAAAITAWWTTAAAAAWAAIGWTTTWTAAAITWWGTTAWTITTTATTTTWAAAITG 938
                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTTTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTT 413
                                                                 AAAAAATAWTAAAAWARTKKTGTRTWTKWAAAAAAAAAAAWWKGGKGGKKKTKGGGGGKG
                                                                                                                      TAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGGGATAGG 370
                                                                                                                                                                                       TATATAAAAAWWATTATGTATAWWAAATRTWWTGTATTKAAAATATWGRATATTKAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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1 (bases 1 to 1101)
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/note="end : TET3"
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/db_xref="taxon:7227"
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36.2%;
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RKRADDKRDAADDRDDAATWTTWTTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDRDR
                                                                                                                                                                                                                                             AAGGGGTTTTTATGAATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTA
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                                              TTTATGAAACTAATAAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGT
                                                                                                  WADADWWTWDAAADDWWADDRWDAWAWKWDDAWAWGARTADRRDWGDRAGKRGGARKRRD
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
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AL063971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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/note="end : TET3"
64 c 131 g
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/db_xref="taxon:7227"
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Pred. No. 0.0024;
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                                                                                                                                                                                                                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila bha provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                 /clone_lib="RPCI-98"
/note="end : TET3"
164 c 81 g
                                                                                                                                                                            /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                                                                                                                                1. .996
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Score 69.6; DB 17; Length 996; Pred. No. 0.0061;
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Query Match Best Local Similarity

9.3%;

Matches

164;

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65;

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224;

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                                                                                                                                                                                                                                                                                                d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector {\bf r}
                                                                                                                                                                                                                                                                                                                                                                       Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part
Determination with the European Drosophila Genome Project (EDC
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
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Direct Submission
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS0100X 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03G04 of DrossBAC library from Drosophila melanogaster (fruit
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                                                                              /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                              /clone="BACN03G04"
/clone lib-">
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                     Location/Qualifiers
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Bp 191 91000 EVAL COLUMN BP 191 91000 EVAL COLUMN BP 191 9100 EVAL COLUMN BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton project grant. The DNA was prepared from embryos by Alain Bucheton and the collection of the colle
                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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yeast species
FEBS Lett. 487
20584711
11152876
                                                                                                                                                                                                                                                                                                                                                                                           Yarrowia lipolytica.
Yarrowia lipolytica
                                                                            Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts:
yeast species for molecular evolution studies
                                                                                                                                                                                Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., Bechtigny, J., Dujon, B., Durrens, P., Lepingle, A., Llore Malpertuy, A., Neuveglise, C., Becker, Kalogeropoulos, O., Cantin W., Totala F., Totala, C., Cantin W., Cantin W., Totala F., Totala, C., Cantin W., Ca
                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
1 (bases 1 to 1013)
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AL412260
AL412260.1 GI:12182622
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T7 end of clone AWOAA016E05 of library AWOAA from strain CLIB 89
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/clone_lib="ProsBAC"
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/db_xref="taxon:7227"
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DEFINITION

CNS01G8P 910 bp DNA linear GSS 01-JUN-2001 Anopheles gambiae GSS SP6 end of clone 06E14 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),

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                                                                        TCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGGGATAGGTTCTTTTGCTCAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Casaregola, S., Neuveglise, C., Lepingle, A., Bon, E., Feynerol, C., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/clone="AWOAAO16EO5"
/clone_lib="AWOAA"
/note="end : T7"
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/strain="CLIB 89"
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                                                                                                                                                                                                                                           Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pteryo
Eukaryota; Endopterygota; Diptera; Nematocera; Culicoidea
Drosophila melanogaster genome survey sequence BACR29B23 of RPCI-98 library from Drosophila me
                                   CNS00EVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 910)
Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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AL142826.1 GI:7000944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Anopheles gambiae"
/strain="pEST"
/db_xref="taxon:7165"
/clone="06E14"
/clone_11b="NotreDame1"
/note="end : SP6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGS. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                       GGGTTAATACTTACAGGAGCTTATTTGGACATCAAGGATTTTGATAATAATGCTAAAAAA 494
                                                                                                                                    AATAAGTTTTTAATTTTTATTTTGGTAATCTTTTGTGCTTTTTCTAGTTTTTGCTCAAGAT 254
                                                AAGAAAGATTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGGGATAGGTTCT 374
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                                                                                         TTTGCTCAAGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATA 434

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence. AL069706
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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/db_xref="taxon:7227"
/clone="BACR29B23"
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                                                                                                                                                                                                                                              TTTTTTAAAWWAWATWATATTATTTAATTWATT-----TAATWTATTTAYTTTA 1028
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                                                                                         WTTTTTKKMAVADTWCMMAAWAAMAAAHHWWWAWTWTTTYMNAAWAAAAAAAATAWWWYC 908
                                                                                                                                                    GTTTTGCTCAAGATGATTCTAAAAGCACTTTTAATCTGGGAGCGGGAGAAAAATTTTTTGG
                                                                                                                                                                                                               AAWTTTTYWVAATKATAWAAWWTTTTTTTTTTTTTHTSYTYWWAATTTTTTTTTTTYTTY 968
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project (EDGP) - The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project (EDGP) - The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and the provided by a MRC project grant gran
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                     BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@enoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
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Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Reptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                   and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-JUN-1999) Genoscope - Centre
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                                                                                                                    This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                   Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1092)
Roest-Crollius, H., J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL175696.1 GI:7813753
GSS; genome survey seq
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                                                                                                                                                                                                                                                                                                                                            Unpublished
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                          /organism="Tetraodon nigroviridis'
/db_xref="taxon:99883"
/clone="222L11"
/clone=lib="G"
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169 c 165
                                                                                                      ocation/Qualifiers
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Quetier,F., Saurin,W.,
sequence
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             This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
 Location/Qualifiers
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ORIGIN
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1 (bases 1 to 1038)

Roest-Crollius, H., Jaillon, O., Dasilya, C., Bouneau, L., Fisher, C.,
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Tetraodon nigroviridis genome survey sequence T7
194P16 of library G from Tetraodon nigroviridis,
                                                                                                                                        Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Ja
                                                                                                                                                                                                                                                  Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                      Human gene number estimate
Tetraodon nigroviridis DNA
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GSS; genome survey sequence
Tetraodon nigroviridis.
                                          Submitted (12-APR-2000)
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                                                               Direct Submission
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                                                                                                                                                                                       Weissenbach,J
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35.8%;
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr

BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila delanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Billaud at CEPH (Centre Library CDros BAC) was made by Alain Bil
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                           d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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GSS.
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                        /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
a 172 c 106 g
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/db_xref="taxon:99883"
/clone="194P16"
/clone_11b="G"
/note="Genoscope sequence ID : COA
152 c 183 g 145 t 186
                                                                                                                                                            /db_xref="taxon:72"
/clone="BACN15A12"
                                                                                                                                                                                                  /organism="Drosophila
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                Location/Qualifiers
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survey sequence T7 end of BAC
rom Drosophila melanogaster (fruit
                           316
                                                                                                                                                                                                                              melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS; genome survey sequence
Tetraodon nigroviridis
Tetraodon nigroviridis
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                 Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon
                                                                          Genoscope.
Direct Submission
                                                                                                                                                                                                     Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                         Submitted (12-APR-2000)
                                                                                                                              Unpublished
                                                                                                                                                                                         Weissenbach,J.
                                                                                                                                                                                                                                                                                                                   Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                   Roest-Crollius, H., Jaillon, O., Dasilva, C., Bernot, A., Fizames, C., Wincker, P., Brottie
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Pred. No. 0
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                 part of a large
nigroviridis
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                                                                                                                                                                                                                                                                                                                                                          Fisher, C.,
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Best Local Similarity 41.5
Matches 176; Conservative
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                 443 ACTT 446
                                                                      547 TTTT 550
                                   383 AGGAGATATCCTTGGAGGTTCTCTTATTCTTGGATTTGATGCGGTTGGTATAAGGGTTAAT 442
                                                                                                            323 TTCTCTTGTACCATTTTTATTGAACCTTTTTTTAGGGTTCGGGATAGGTTCTTTTGCTCA 382
                                                                                                                                                                                                                                                                  23 TATTGTTAAAAGAATTGAAATTGCTAATTTTATGGTTAAATCAAGAAGCTCTATTGGTAA 82
                                                                                                                                                                                                                                         83 GCGAATTTCGAGTAACAATTTGAAAAAGTTAAATTTTAAATAGTTCCAAAAGCCTTTTTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       8.3%; Score 62; DB 17; Length 576; 41.5%; Pred. No. 0.16;
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Search completed: March 27, 2003, 03:54:20 Job time : 1058.13 secs